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MPSrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Fri Oct 1 13:56:03 1999; MasPar time 28.46 Seconds
411.665 Million cell updates/sec
Tabular output not generated.

Title: >US-09-026-400-4
Description: (1-551) from US09026400.pep
Perfect Score: 3749
Sequence: 1 MATVRQSDGVAANGLAFAA.....LGRKSFQQRNKRNSDDC 551

Scoring table: PAM 150
Gap 11

Searched: 170751 seqs, 2126608 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseq35
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part32 33:part33
34:part34 35:part35 36:part36 37:part37 38:part38
39:part39

Statistics: Mean 35.992; Variance 182.932; scale 0.197

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	3749	100.0	551	34	Nicotianamine aminotr	2.58e-301
2	2888	77.0	461	34	Nicotianamine aminotr	1.97e-228
3	402	10.7	394	26	Aquifex aspartate ami	3.44e-21
4	269	7.2	398	26	Ammonifex degensli as	7.20e-11
5	259	6.9	373	26	Aquifex aspartate ami	4.11e-10
6	230	6.1	482	26	Barley alanine aminot	6.10e-08
7	229	6.1	517	20	Carnation ACC synthas	7.24e-08
8	213	5.7	422	17	Human kynurenine amin	1.10e-06
9	207	5.5	423	17	Rat kynurenine aminot	3.02e-06
10	207	5.5	437	17	Rat kynurenine aminot	3.02e-06
11	207	5.5	457	17	Rat kynurenine aminot	3.02e-06
12	196	5.2	493	5	ACC synthetase.	1.90e-05
13	186	5.0	175	2	Peptide antigenic for	9.99e-05
14	189	5.0	429	1	Antigenic protein for	6.08e-05
15	186	5.0	486	23	Poplar 1-aminocyclopr	9.99e-05
16	186	5.0	493	29	Zucchini ACC synthase	9.99e-05

17	186	5.0	493	3	R15505	Zucchini ACC synthase	9.99e-05
18	187	5.0	496	7	R35231	Rat ALT.	8.47e-05
19	185	4.9	493	29	W47310	Protein encoded by zu	1.18e-04
20	185	4.9	493	3	R15504	Zucchini ACC synthase	1.18e-04
21	180	4.8	936	39	W89801	Staphylococcus aureus	2.68e-04
22	175	4.7	480	32	W60239	Rose 1-aminocycloprop	6.07e-04
23	177	4.7	494	29	W47312	Zucchini ACC synthase	4.38e-04
24	177	4.7	494	3	R15863	Zucchini ACC synthase	4.38e-04
25	171	4.6	362	20	W04559	Carnation ACC synthas	1.16e-03
26	171	4.6	493	7	R35230	Human ALT.	1.16e-03
27	172	4.6	495	30	W46904	A human mutant alanin	9.90e-04
28	172	4.6	496	34	W62267	Modified human alanin	9.90e-04
29	167	4.5	469	3	R15510	Tomato ACC synthase e	2.23e-03
30	168	4.5	980	14	R81318	Adhesion protein.	1.89e-03
31	167	4.5	1059	1	P82962	SEPI4 protein compris	2.23e-03
32	170	4.5	1092	29	W41602	Staphylococcus epidei	1.37e-03
33	166	4.4	402	2	P70709	Plasmodium cynomolgi	2.62e-03
34	164	4.4	1038	19	R95107	Fibronectin cell bind	3.61e-03
35	161	4.3	481	23	W21754	Poplar 1-aminocyclopr	5.85e-03
36	160	4.3	695	31	W53526	Amino acid sequence o	6.87e-03
37	161	4.3	1023	31	W53524	Amino acid sequence o	5.85e-03
38	161	4.3	1059	8	R41013	SLP4 multimeric prote	5.85e-03
39	161	4.3	1059	24	W26348	SLP4 synthetic protei	5.85e-03
40	163	4.3	1177	24	W26342	Silk-like protein Slp	4.24e-03
41	163	4.3	1177	1	P80940	SLP4 protein compri	4.24e-03
42	163	4.3	1177	19	R95105	Silk like protein (SL	4.24e-03
43	163	4.3	1177	1	R05307	SLP III (Silk-fibroin	4.24e-03
44	163	4.3	1178	32	W53518	Amino acid sequence o	4.24e-03
45	163	4.3	1178	8	R41007	Silk-like protein Slp	4.24e-03

ALIGNMENTS

RESULT 1
ID W61643 standard; Protein; 551 AA.
AC W61643.
DT 27-OCT-1998 (first entry)
DE Nicotianamine aminotransferase 58148.62 molecular weight protein.
KW Nicotianamine aminotransferase; plant; iron absorption;
OS Iron deficiency chlorosis.
OS Gramineae sp.
PN EP-860499-A2.
PD 26-AUG-1998.
PR 19-FEB-1998; 102891.
PR 21-FEB-1997; JP-037499.
PA (SUMO) SUMITOMO CHEM CO LTD.
PI Mori S, Nakanishi H, Takahashi M;
DR WPI: 98-439341/38.
DR N-P5DB; V48148.
PT New nicotianamine aminotransferase protein and DNA - useful for
PT enhancing iron absorption of plant cells
PS Claim 3; Page 14-15; 17pp; English.
CC The nicotianamine aminotransferase can be used in a plasmid to transform
CC plant cells to produce cells with enhanced iron absorption, and it is
CC implied [though not stated] that plants with improved resistance to iron
CC deficiency chlorosis in calcareous soils can be regenerated from the
CC transformed cells. The gene fragment can be used to detect, amplify
CC and/or isolate nicotianamine aminotransferase genes.
SQ Sequence 551 AA;

Query Match 100.0%; Score 3749; DB 34; Length 551;
Best Local Similarity 100.0%; Pred. No. 2.58e-301;
Matches 551; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db	1	matvrqsdgvaanglavaaaangksngghvaavngksngghvgdangksngghvaada	60
QY	1	MATVRQSDGVAANGLAFAAANGKSNHGVAANGKSNHGVDADANGKSNHGVAADA	60
Db	61	ngksngghaetanghgeatgktngtngresngghaadaangneshaedsaangesnha	120
QY	61	NGKSNGHAEATANGGEATANGKTNGHRESNGHAEAAANGESHAEDSAANGESNHA	120
Db	121	aaaaaeavvfnfagdkgvlvaatgamsirairkyiasvqekgprvpilahgdpsv	180

Query Match	77.0%	Score 2888;	DB 34;	Length 461;
Best Local Similarity	88.1%	pred. No. 1.97e-228;		
Matches	409;	Conservative 30;	Mismatches 20;	Indels 5; Gaps 1;
Db	3	hqsngheaaaaaangksnghaaazngksnghaaaaa-----vewfargkgdglattga	57	
QY	88	RESNGHAERADANGESNEHAEDSAANGESNGHAAAAEEAAVEWNFACGKGVLAATGA	147	
Db	58	knsirairykasveesgprvplahgdpsvfpafrtaveaedavaaalrtgqfncya	117	
QY	148	NMSIRAIRYKISASVOEKGRPVLPVLAHGDPSVFPAPFRTAVEAEDAVAAAVRTGQNCYP	207	
Db	118	agvglpaarsavaehlsqgvpvylsaddvfltaggtgaievlpvlaqtaganillprpg	177	

	Query Match	10.7%	Score 402;	DB 26;	Length 394;
	Best Local Similarity	28.2%	Pred. No. 3,44e-21;		
	Matches	103;	Conservative 95;	Mismatches 139;	Indels 28; Gaps 26;
Db	42 pfditpdfikeaciralrgqtkk-yapsagipelrealtaekllkenveyk-pseiv-vs	98	: : : :		
QY	182 PAFRTVEAEADVAAAVRIGQFCNCPAGVGLTFAARSAVAEHL-SQG-VPMUSADDDVFUT	239	: : : :		
Db	99 agakmvlifmailde--gdevilpspywvtypedigrfggvpv-evplkkekgfqisl	155	: : : :		
QY	240 AGGTQAI-EVIIIPVLAQTAGANILLPRPCPNYEARAAP-NRLVRHFDDLDPKGWEIDI	297	: : : :		
Db	156 edvk'ekvter-tkaivinspnntgavveeeelkkiaefcvar-gifiisdecyeyfyvg	213	: : : :		
QY	298 DSI-ESIAKNTMTAMVIINPNCPSGYSDHLSKAQEV-AKRLLGTLTADEYQKLVLG	355	: : : :		

26 MAY-1996; AU0286.
09-MAY-1995; AU-002862.
(ALLR-) ALLRAD NO 1 PTY LTD.
(FLOR-) FLORIGENE INVESTMENTS PTY LTD.
Cornish EC, Graham MW, Guttererson NI,
Tucker WT;

Isolated DNA encoding mammalian kynurenine amino:transferase (KAT) can be inserted into vectors and subsequently cells can be used for gene therapy. The vector and host cells can be used for cerebral implantation to where KAT can directly catalyse the production of Example 4; Figure 4; 51pp: English.

PN WC90U19933-AL.
 PD 25-JAN-1996. U07855.
 PF 23-JUN-1995; U07855.
 PF 07-JUL-1994; US-271667.
 PA (PHAA) PHARMACIA SPA.
 PA (UYUA-) UNIV MARYLAND BALTIMORE.
 PI Benatti L, Breton J, Mosca M, Okuno E, Schwarcz R;
 PI Speciale C;
 DR WPI: 96-097623/10.
 DR N-PSDB: T11743.

PT Isolated DNA encoding mammalian kynurenine amino-transferase (KAT) -
 PT useful in gene therapy applications and for identifying KAT in brain
 PT tissue

PS Claim 16; Figure 4; 51pp; English.
 CC Sequences encoding kynurenine aminotransferase (KAT) can be inserted
 CC into vectors and subsequently cells and hence can be used for gene
 CC therapy. The vector and host cells can be used for cerebral
 CC implantation to where KAT can directly catalyze the production of
 CC kynurenine acid (KYNA) from kynurenine (KYN). It is thought KYNA acts
 CC as a negative endogenous modulator of cerebral glutamatergic
 CC function. KYNA concentrations and the activity of KAT show an
 CC increase with age. KAT inhibitors, by providing an increase of the
 CC glutamatergic tone at the NMDA receptor, could be useful in
 CC situations where NMDA receptor function is insufficient and/or KAT
 CC activity and KYNA levels are abnormally enhanced. Hence they could
 CC be particularly useful in the treatment of the pathological
 CC consequences associated with the aging processes in the brain.
 CC Three KAT clones are described in T11560, T11742-43.
 SQ Sequence 457 AA;

Query Match 5.5%; Score 207; DB 17; Length 457;
 Best Local Similarity 33.0%; Pred. No. 3.02e-06;
 Matches 35; Conservative 24; Mismatches 46; Indels 1; Gaps 1;

Db 188 lgsandwqlpaelskftprtkvlnvntpnplgkvfsmlelelvancqghdvcsid 247

QY 287 LIPDKGWEIDIDSLSDAKNTAMVIINPNPNCVSVSYDHLKVAEAKRLGILVIAD 346

Db 248 evyqvlvdyghvhsiaslpgmwdrtltigsagksfsatgkwgvw 293

QY 347 EYIGKLVLSGAPFIPMGVFGHI-TPVLSIGLSKSWIVPGWRLGW 391

RESULT 12

ID R25406 standard; Protein; 493 AA.

AC R25406;

DT 18-JAN-1993 (first entry)

DE ACC synthetase.

KW 1-aminocyclopropane-1-carboxylic acid synthetase; detriment;

KW ethylene; growth; maturity; aging; plant.

OS Cucurbita maxima.

PN J04169183-A.

PD 17-JUN-1992.

PF 31-OCT-1990; 296943.

PR 31-OCT-1990; JP-296943.

PA (SUMO) SUMITOMO CHEM CO LTD.

DR WPI; 92-253389/31.

DR N-PSDB; Q25896.

PT Detriment induced ACC synthetase gene - used for control of
 PT bio-synthesis of ethylene, for controlling growth, maturity and
 PT ageing of higher plant

PS Claim 2; Fig 1; 10pp; Japanese.

CC The protein sequence was deduced from the DNA sequence of the gene
 CC encoding detriment induced 1-aminocyclopropane-1-carboxylic acid
 CC (ACC) synthetase (EC 4.4.1.14) which was obtd. by screening a cDNA
 CC library prepd. from Cucurbita maxima mRNA. EC4.4.1.14 obtd. from
 CC cDNA library clones was screened by an antibody method to identify
 CC colonies producing EC 4.4.1.14, e.g. E.coli DH5 alpha/PCMW33.

CC Biosynthesis of ethylene is controlled by ACC synthetase. Ethylene
 CC controls the growth, maturing and aging of higher plants.

SQ Sequence 493 AA;

Query Match 5.2%; Score 196; DB 5; Length 493;

Best Local Similarity 24.3%; Pred. No. 1.90e-05;

Matches 87; Conservative 101; Mismatches 140; Indels 30; Gaps 23;

Db 97 glpefrngiasfmgkvrgrvafpsrvimgggatgasvtficlad-pgdaflypspy 155

QY 211 GLPAARSAVAEHLs--QGVYPVMSLADDDVLTAGTQAEIVIPVLAQTAGANILLPRPY 268

Db 156 aafdrldkwrtraqirvhnchsnfnqvtkaalelaykkaeanikvkgviitnpsnplg 215

QY 269 PNTEARAAP-NRLEVRHFDLPDKGWEIDIDSLE-SI--A-DKNTAM-VII-NPNNPCG 321

Db 216 ttdrdrtkltvtfvngdhidhlcideiysatvfkaptffisiagievneehcklelihly 275

QY 322 SVYSYDHLKSKVAEAKRLGILVIADVYGVKLVGSAPFIPMG--V--PGHITPVL-SIG- 375

Db 276 slskdmglpgfrvg-i-iysyndvv--vrrarqmssfglvssqtghllaamlsd--edfv 329

QY 376 SLRSKSWIVPGWRLGVAVYDPRKILQETKISTITNVLNVSTDPATFQAALPQILENTK 435

Db 330 dkflaenskrilaerharftkel-dkmgitclnsnag-vfvvmdlr-rlkqdtkaemel 386

QY 436 EDFTKAIIIGLKESEICYKOIKENKYITCPEKPEGSFVMVKLNLHL-EE-IDDIDIF 493

Db 387 wrvlinevklvsgssfhvtepgwfrvcfanmddntvdvalnrhsvfenidkkn 444

QY 494 CKLAKEESVILCPGSLGMAN--WWRITFACVP--SSLQDGLGRIKSPCQRKNRSS 548

RESULT 13

ID R08261 standard; protein; 175 AA.

AC R08261;

DT 18-FEB-1991 (first entry)

DE Peptide antigenic for malarial antiporozoite Antibodies.

KW Malaria; vaccine; universal carrier molecule.

OS Synthetic.

PH Key Location/Qualifiers

FT duplication 1..160

FT /label= (-Asn-Ala-Ala-Gly-)3-40

FT duplication 161..175

FT /label= (-Lys-)1-15 (odd number)

FT cross_links 161..175

FT /label= nth Lys has side chain identical to

FT AAs 1..n-1

PN EP-398443-A.

PD 22-NOV-1990.

PF 16-MAY-1990; 201244.

PR 19-MAY-1989; IT-020553.

PR 23-MAR-1990; IT-019800.

PA (ENIE) ENIRICERCH SPA.

PI Pessi A, Bonelli F, Chiappinelli L, Bianchi E, Del Giudice G;

DR WPI; 90-350221/47.

PT New immunogenic cpds. for synthetic vaccines for Plasmodium

PT malariae - and for determ. of antibodies of Plasmodium malariae

PS Claim 1; Page 15; 19pp; English.

CC Peptides have a fractal structure, branching at each lysine residue

CC into a side chain identical to all AAs at its N-terminal.

CC Peptides are useful as universal carrier molecules inducing

CC genetically unrestricted protective immunity against different

CC pathogenic agents.

CC Specifically, the peptides may be used as antigens in vaccination

CC and immunoassay of Plasmodium malariae antiporozoite antibodies.

CC See also R08260.

SQ Sequence 175 AA;

Query Match 5.0%; Score 186; DB 2; Length 175;

Best Local Similarity 32.0%; Pred. No. 9.99e-05;

Matches 40; Conservative 42; Mismatches 38; Indels 5; Gaps 5;

Db 2 aagnaagnaagnaagnaagnaagnaagnaagnaagna--gnaagnaagna--agnaagna 59

QY 7 SDGVAANGLAVAAAANGKSNHGVA--VNGKSNHGVDADANGKSNHGVAADANGKSN 65

Db 60 gnaagnaagnaagnaagnaagnaagnaagnaagnaagna--gnaagnaagna--gnaagna 118

QY 66 GHAEATANGHGEATANGKTNHRESNGHAEAA--DANGESHAEDSANGESNGHAAAA 124

Db 119 agnaa 123

QY 125 EEEA 129

RESULT 14

ID P90064 standard; protein; 429 AA.

P90064;
AC 1-NOV-1989 (first entry)
DE Antigenic protein for malaria vaccination
KW Antigenic; vaccine; Plasmodium malariae;
KW circumsporozoite protein.
OS Plasmodium malariae
PN U5738746-A.
PD 16-MAY-1989.
PF 31-AUG-1988; 238746.
PR 31-AUG-1988; US-238746.
PI (USHS) Nat Inst of Health.
PA Lal A;
DR WPI; 89-172958/23.
PT Antigenic protein for vaccination against malaria
PT - encoded by cloned gene coding for Plasmodium
PT malariae circumsporozoite protein.
PS Disclosure; fig 1; 11pp; English.
CC Antigenic circumsporozoite protein of Plasmodium malariae. Used
CC as a vaccine against malaria.
SQ Sequence 429 AA;

Query Match 5.0%; Score 189; DB 1; Length 429;
Best Local Similarity 28.0%; Pred. No. 6.08e+05;
Matches 45; Conservative 53; Mismatches 57; Indels 6; Gaps 3;

Db 175 agnaagaaagndagnaagaagaaagaaagaaagaaagaa-gnaagaaagaa-agnaagaa 232
QY : ||| |::||| |::||| |::||| |::||| |::||| |::||| |::||| |:
7 SDGVAANGLAFAAAAGKSGHGVAAA-VNKGNGHGVDADANGKSGHVADANGKSN 65

Db 233 gnaagaaagaaagaaagaaagaaagaaagaaagaaagaaagaa-gnaagaaagaa 291
QY |:| |::||| |::||| |::||| |::||| |::||| |::||| |:
66 GHAEATANGGEATANGKTNGHRSHGAFAA-DANGESNEHAEDSAANGESNHAAAA 124

Db 292 agnaagaaagaaagaaagaaagaaakka-knkdknvdatnkk 331
QY : |::||| |::||| |::||| |::||| |:
125 EEEEEVEWNPAGAKDGLAATGANMSIRAIRYKISASVQEK 165

RESULT 15
ID W21755 standard; Protein; 486 AA.
AC W21755;
DT 16-SEP-1997 (revised)
DT 26-AUG-1997 (first entry)
DE Poplar 1-amino cyclopropane-1-carboxylic acid synthase PNACS2.
KW Ozone; induction; exposure; resistance; transgenic plant; ACC;
KW 1-amino cyclopropane-1-carboxylic acid biosynthesis.
OS Populus nigra.
PN J09075088-A.
PD 25-MAR-1997.
PF 07-SEP-1995; 254510.
PR 07-SEP-1995; JP-254510.
PA (TOYT) TOYOTA JIDOSHA KK.
DR WPI; 97-239270/22.
DR N-PDSB; T73502.
PT Ozone-induced 1-amino:cyclopropane-1-carboxylic acid synthetic
PT enzyme genes - from poplar tree, are useful for generating
PT ozone-resistant trees and pollution clean-up trees
PS Claim 2; Pages 9-11; 12pp; Japanese.

CC This protein is a 1-amino cyclopropane-1-carboxylic acid (ACC) synthase
CC encoded by a cDNA clone isolated from poplar trees which
CC had been exposed to ozone. Exposure conditions were: 0.1 ppm ozone
CC for 6 hours after one hour acclimation at 25 degrees C, 70 % relative
CC humidity, 30 k lux and air current 30 cm/second. The gene will be
CC useful for breeding air pollutant ozone-resistant trees, especially
CC poplar.
CC (Note: Record has been revised in order to correct the Organism
CC Source field).
SQ Sequence 486 AA;

Query Match 5.0%; Score 186; DB 23; Length 486;
Best Local Similarity 26.3%; Pred. No. 9.99e+05;
Matches 94; Conservative 89; Mismatches 144; Indels 30; Gaps 22;

MAISRELA (TM)

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MPSrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Oct 1 13:55:14 1999; MasPar time 26.02 Seconds
Tabular output not generated. 848.473 Million cell updates/sec

Title: >US-09-026-400-4
Description: (1-551) from US09026400.pep
Perfect score: 3749
Sequence: 1 MATVRQSDGVAANGLAVAAA.....LGRIKFCQNRKRRSSDDC 551

Scoring table: PAM 150
Gap 11

Searched: 122810 seqs, 40068593 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: pir60
1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 50.754; Variance 128.964; scale 0.394

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description	Pred. No.
1	952	25.4	454	1	tyrosine transaminase	1.52e-126
2	921	24.6	454	2	tyrosine transaminase	1.61e-121
3	489	13.0	429	2	probable aspc protein	7.03e-53
4	457	12.2	401	2	probable aspartate am	5.78e-48
5	402	10.7	394	2	aspartate aminotransf	1.30e-39
6	399	10.6	405	2	hypothetical protein	3.67e-39
7	374	10.0	402	2	aspartate transaminas	2.03e-35
8	370	9.9	375	2	aspartate transaminas	8.01e-35
9	359	9.6	379	2	hypothetical protein	3.44e-33
10	355	9.5	357	2	aspartate aminotransf	1.35e-32
11	353	9.4	390	2	hypothetical protein	2.66e-32
12	349	9.3	390	2	aspartate aminotransf	1.04e-31
13	344	9.2	392	2	aspartate transaminas	5.85e-31
14	323	8.6	379	2	aspartate aminotransf	6.71e-28
15	323	8.6	391	2	probable aspartate am	6.71e-28
16	319	8.5	393	2	aspartate aminotransf	2.56e-27
17	301	8.0	392	2	probable aspartate tr	1.03e-24
18	298	7.9	412	2	aspartate aminotransf	2.77e-24
19	294	7.8	374	2	aspartate aminotransf	1.04e-23
20	287	7.7	400	2	aspartate transaminas	1.04e-22
21	288	7.7	507	2	probable membrane pro	7.46e-23
22	289	7.7	592	2	probable membrane pro	5.37e-23
23	283	7.5	383	2	aspartate transaminas	3.84e-22

24	272	7.3	389	2	E71009	probable aspartate am	1.38e-20
25	274	7.3	432	2	F64484	alanine transaminase	7.28e-21
26	270	7.2	385	2	JC4537	aspartate transaminas	2.65e-20
27	271	7.2	390	2	F69452	aminotransferase (Asp	1.92e-20
28	259	6.8	373	2	E70338	aspartate aminotransf	9.21e-19
29	255	6.8	389	2	S74343	aspartate aminotransf	3.32e-18
30	253	6.7	444	2	S56832	kyurenine aminotransf	6.29e-18
31	248	6.6	373	2	F69545	aspartate aminotransf	3.10e-17
32	248	6.6	389	2	S75949	hypothetical protein	3.10e-17
33	247	6.6	410	2	A40658	aspartate transaminas	4.28e-17
34	240	6.4	386	2	F64793	ybdL protein - Escher	3.90e-16
35	234	6.2	516	2	S19252	1-aminocyclopropane-1	2.58e-15
36	234	6.2	518	2	S31442	1-aminocyclopropane-1	2.58e-15
37	227	6.1	390	2	D70849	probable aminotransf	2.29e-14
38	230	6.1	401	2	S75385	probable aspartate tr	9.01e-15
39	230	6.1	482	2	S42535	alanine transaminase	9.01e-15
40	219	5.8	399	2	S39740	aspartate aminotransf	2.73e-13
41	218	5.8	482	2	S28429	alanine transaminase	3.72e-13
42	212	5.7	388	2	C70605	probable aminotransf	2.34e-12
43	212	5.7	412	2	H65011	hypothetical protein	2.34e-12
44	213	5.7	422	2	S52790	glutamine-phenylpyru	1.72e-12
45	214	5.7	465	2	H69777	transcription regulat	1.27e-12

ALIGNMENTS

RESULT	1
ENTRY	XNRTY
TITLE	tyrosine transaminase (EC 2.6.1.5) - rat
ALTERNATE_NAMES	tyrosine aminotransferase
ORGANISM	#formal_name Rattus norvegicus #common_name Norway rat
DATE	30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 26-Feb-1999
ACCESSIONS	A23310; A31804; JN0343; A48430; S18308; S17849
REFERENCE	A23310
#authors	Grange, T.; Guenet, C.; Dietrich, J.B.; Chasserot, S.; Fromont, M.; Befort, N.; Jami, J.; Beck, G.; Pictet, R.
#journal	J. Mol. Biol. (1985) 184:347-350
#title	Complete complementary DNA of rat tyrosine aminotransferase messenger RNA. Deduction of the primary structure of the enzyme.
#cross-references	MUID:85293103
#accession	A23310
#molecule_type	mRNA
#residues	1-454
#label	GRA
#cross-references	EMBL:X02741; NID:g57327; PID:g57328
#note	part of this sequence was confirmed by protein sequencing
REFERENCE	A31804
#authors	Hargrove, J.L.; Scoble, H.A.; Mathews, W.R.; Baumstark, B.R.; Biemann, K.
#journal	J. Biol. Chem. (1989) 264:45-53
#title	The structure of tyrosine aminotransferase. Evidence for domains involved in catalysis and enzyme turnover.
#cross-references	MUID:89079691
#accession	A31804
#molecule_type	mRNA
#residues	226-284
#label	'G', '286-358', 'DL', '361-444', 'D', '446-454' #label HAR
#cross-references	GB:M18340
#note	the authors translated the codon GGG for residue 285 as pro
#note	part of this sequence was confirmed by protein sequencing
REFERENCE	JN0343
#authors	Zelenin, S.M.; Popova, V.S.; Morozov, I.V.; Tishkav, V.I.; Egorov, A.M.; Mervetsov, N.P.
#journal	Bioorg. Khim. (1991) 17:994-996
#title	Nucleotide sequence of an EcoRI-fragment of the rat tyrosine aminotransferase gene determined on the automated sequencer "Applied Biosystems" model 370A.
#cross-references	MUID:92172066
#accession	JN0343
#molecule_type	DNA

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#residues      385-454 #label ZEL
##experimental_source liver
REFERENCE A48430
#authors Morozov, I.V.; Mishin, V.P.; Zelenin, S.M.; Popova, V.S.; Mervetsov, N.P.
#journal DNA Seq. (1990) 1:151-155
#title Nucleotide sequence of rat liver tyrosine aminotransferase gene fragment.
#cross-references MID:92190544
#accession A48430
##status preliminary
##molecule_type DNA
##residues 190-284,'L',286-386 ##label MOR
##cross-references GB:X1590; NID:957845; PID:g1334238
##experimental_source liver
##note sequence extracted from NCBI backbone (NCBIN:89708, NCBIP:89709)

REFERENCE SI8308
#authors Lorber, B.; Dietrich, J.B.; Kern, D.
#journal FEBS Lett. (1991) 291:345-349
#title Isolation and characterization of active N-terminal truncated apo- and holoenzyme of mammalian liver tyrosine aminotransferase.
#cross-references MID:92038067
#accession SI8308
##molecule_type protein
##residues 38-52;58-81 ##label LOR
##experimental_source liver
REFERENCE SI7849
#authors Dietrich, J.B.; Lorber, B.; Kern, D.
#journal Eur. J. Biochem. (1991) 201:399-407
#title Expression of mammalian tyrosine aminotransferase in Saccharomyces cerevisiae and Escherichia coli. Purification to homogeneity and characterization of the enzyme overproduced in the bacteria.
#cross-references MID:92037592
#accession SI7849
##status not compared with conceptual translation
##molecule_type DNA
##residues 1,'V',3-10 ##label DIE
##experimental_source liver

GENETICS 408/3
#introns
CLASSIFICATION superfamily mammalian tyrosine aminotransferase acetylated amino end; aminotransferase; homodimer; phosphoprotein; pyridoxal phosphate
KEYWORDS
FEATURE 383-394
1    #region PST sequence\
     #modified_site acetylated amino end (Met) #status experimental\
     #binding_site pyridoxal phosphate (tyr) (covalent) #status experimental
SUMMARY #length 454 #molecular-weight 50635 #checksum 7044

Query Match          25.4%; Score 952; DB 1; Length 454;
Best Local Similarity 34.8%; Pred.No.1.52e-126;
Matches 139; Conservative 120; Mismatches 130; Indels 11; Gaps 10;

Db   49  SNKTFNPIRAIVDNMKVPNPNTKVISLSIGDPTVFGNLPDTPEVTQAMKDALDSGRYNG 108
     :|::: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |::
Qy   147 ANMSIRAIRKYISA-SVEQKGPPVLPLAHGDPSPFAFRFAEADVAARVGTGFQFNC 205
     :|::: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |::
Db   109 YAPSIGYLSSREEVASYYHCHEAP--LEAKDVILTSGCSQAIEICLVLAN-PGONTILP 165
     :|::: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |::
Qy   206 YPAGVGGLPAARSAAAEHL-SQGVPYMLSDADVLTAGGTQTAEIPIPVLAOTAGANILLP 264
     :|::: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |::
Db   166 RPFSLRYTLAESMGTEVKLYNLPLLPEKSWEIDLKOLESILDSEKTACLVNNPNPCGSVF 225
     :|::: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |::
Qy   265 RPGPVNEYAARNREVRHFDLIIDPKGWEDIDSLESTADKNITTAWIIINPNPCGSVI 324
     :|::: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |::
Db   226 SKRHLOKITAVARQCVPILADEIFYGDVMFSCKYEPLANISTNVPIILSCGGIAKRMLVP 285
     | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qv   325 SYDLHSKVAEVAKRLGITLVADSYGVKLVLGSAFTPGMFGVIFHPVLISGLSKSVTPV 384
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QY	211	GLPAARSAVAEH-LSQGVPYMLSADDFVLTAGGTQAEIVIPVLAQTAGANILLPRGYP	269
Db	156	LWTASTSLAGTGVHY-LCDETOGWQDPIADLESKITER-TKALVINPNPNTGAVTSC	213
QY	270	NYEARAAFNLEVRHFDLIPDK-GWEIDIDSLES-IADKNTAMVINPNPCGSVYSYD	327
Db	214	ILTQWDLARKHOLLADEIYDKILYDDAKHISLASIADPMCLTNGLSKAYRVAGYR	273
QY	328	HLSKVAEVARLGLTVIADDEVYKVLGSAFFIPMGVFGHITPVLSLTSLSKSWIPQWR	387
Db	274	AGWLAIITGPREHASSFTIEGTLNMLRCLNPVPAQHAIOVALGG-HQSI-EDLVLPQGR	331
QY	388	LGVAVYDPRKIILOETKISTINYLVNSYD-PATF-IOAALPOILENTDEFFKAITGL	445
Db	332	L-EORDIAWTKLNEIPGVSCV-KPAGALYAFPRLDPEYD-IDDDEQLVLDLLSEKILV	388
QY	446	LKSESEICYQIKENKVIITCPHRPEGSFMVVKLNLHLLEIDDDIDDFCCCKAEESVIL	505
Db	389	TQGT 392	
QY	506	CPGS 509	
RESULT	4		
ENTRY	D71003	#type complete	
TITLE	probable aspartate aminotransferase - Pyrococcus horikoshii		
ORGANISM	#formal_name Pyrococcus horikoshii		
DATE	14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 14-Aug-1998		
ACCESSIONS	D71003		
REFERENCE	A71000		
#authors	Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekine, M.; Baba, S.; Kotsugi, H.; Hosoyama, A.; Nagai, Y.; Sakai, M.; Ogura, K.; Otsuka, R.; Nakazawa, H.; Takamiya, M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudo, Y.; Yamazaki, J.; Kushida, N.; Oguchi, A.; Aoki, K.; Yoshizawa, T.; Nakamura, Y.; Robb, F.T.; Horikoshi, K.; Masuchi, Y.; Shizuya, H.; Kikuchi, H.		
#journal	DNA Res. (1998) 5:55-76		
#title	Complete sequence and gene organization of the genome of a hyper-thermophilic archaeobacterium, Pyrococcus horikoshii OT3.		
#cross-references	MUID:98344137		
#accession	D71003		
##status	preliminary; nucleic acid sequence not shown; translation not shown		
##molecule_type	DNA		
##residues	1-401 #label KAW		
##cross-references	GB:AF000006; NID:g3236133; PID:d1031371; PID:g3257745		
##experimental_source	strain OT3		
##note	this accession replaces an interim accession for a sequence replaced by GenBank		
GENETICS			
#gene	PH1322		
SUMMARY	#length 401 #molecular-weight 45564 #checksum 5232		
Query Match	12.2%; Score 457; DB 2; Length 401;		
Best Local Similarity	29.0%; Pred. No. 5.78e-48;		
Matches	93; Conservative 83; Mismatches 132; Indels 13; Gaps 12;		
Db	28	LEKKGK-VIRLNTIGDPVKF-DFOPPHMKAEYCAIQEGH-NYIGDSEGLIELREAIK 84	
QY	162	VQEGPRVPLAHGDDSVFPATFAVEADAANAARTGQFNCYPAGVGLPAARSAVAE 221	
Db	85	REKEKNGVDITPDVRYTAATEALQIFGALLD-PGEILIPGSPYPTTGLVKFYGGK 143	
QY	222	HLSQGVPYMLSADDFVLTAGGTQAEIVIPVLAQTAGANILLPRGYPNTVEARAARL 281	
Db	144	PVEYRTIEESGWQPDIDLRKKISER-TKALVINPNPNTGALYDKKTIIEINVAEHD 202	
QY	282	VRHFDLIPDKGWEIDISL-ESADKNTTAMVINPNPCGSVYSYDHLKVAEVARL 340	
Db	203	LVLVSDIEYDLMTYEGKHISP-GLTQDVPVIVNGLSKYVFATGWRILGYMYFVDPGKL 261	

[illegible]

Tomb, J.F.; Adams, M.D.; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glödek, A.; Scott, J.L.; Geohagen, N.S.M.; Weidman, J.F.; Fuhrmann, J.L.; Nguyen, D.; Uitterback, T.R.; Kelley, J.M.; Peterson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, C.A.; Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.R.; Venter, J.C.
#journal Science (1996) 273:1058-1073
#title Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii.
#cross-references UID:9637999
#accession A64300
##status preliminary; nucleic acid sequence not shown; translation not shown
##molecule_type DNA
##residues 1-375 #label BUL
##cross-references GB:U67459; GB:U77117; NID:g1590815; PID:g1592252; TIGR:MJ0001; PID:g1510187
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#map_position REV3343-2216
CLASSIFICATION superfamily aspartate transaminase KEYWORDS aminotransferase
SUMMARY #length 375 #molecular-weight 42395 #checksum 1390
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Df 33 PDFTPKHIIIEAAKRALDEGKTH-YSPNNGIPELREISNKLDYNDVDKNIIVTCG 91 : : : : : : : : : : : : : : : : : : : Qy 182 PAFRTAVEAEADVAARVTGQCNPYPAGVGLPAARSASVAEHL SQGVPMLSADDFLTAG 241 : : : : : : : : : : : : : : : : : : :
Df 92 ASEALMLSTMTLIDR-GDEVLPINPFSVFSETEFAEGRIKNIDL--DENENIDLEKVK 148 : : : : : : : : : : : : : : : : : : : Qy 242 GTQAIEVIIPVLAQTAGANILLPRGPYNPEARAAFNRLVEFRDLIPDKGEWIDISL- 300 : : : : : : : : : : : : : : : : : : :
Df 149 ESIT-KTKYLIFNPSNTGKVYDKETIKGAIEADYNLIIVDSDEVYDKIYYKKHYS 207 : : : : : : : : : : : : : : : : : : : Qy 301 ESIAKDNTAMVVIINFNNPCGSVISYDHL SKVAEAVAKRLGILVIADEVYKGLVLSAPFI 360 : : : : : : : : : : : : : : : : : : :
Df 208 PMQ-PTD-RCIL-INGFSGTYAMTGWRICVLAVSDLNKELDNLNNIKIHQY-SFAC-A 262 : : : : : : : : : : : : : : : : : : : Qy 361 PMGVFGHTIPVLISGLSKSNVIPGWRLGWAVIDP-RKILQTKTISTITNVLVNSTDP 419 : : : : : : : : : : : : : : : : : : :
Df 263 TTFAYGALAA-LRGS-QKCQEDMVREFKRRRDLYINGLKDI-FKV--NKPDGA-FY-I- 314 : : : : : : : : : : : : : : : : : : : Qy 420 ATFIIQ-AALPQLIENTKEFFKAIIIGLLSESSEICYKIENKYITCPHKPEGSFMFWVK 478 : : : : : : : : : : : : : : : : : : :
Df 315 FP-DV-SEVGQGVAKILI-ENKV-LCVPGVAFGENGANYIRFSATKYEDIEKALGII 370 : : : : : : : : : : : : : : : : : : : Qy 479 LNLHLEEIDDDIDFCCKLAKEESVILC-PGSLVG-M-ANWVRITFACVPSSLODGLGRI 535 : : : : : : : : : : : : : : : : : : :
Df 371 K 371
Qy 536 K 536
RESULT 9
ENTRY #type complete
TITLE hypothetical protein Rv0858c - Mycobacterium tuberculosis (strain H37RV)
ORGANISM #formal_name Mycobacterium tuberculosis
DATE 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 17-Jul-1998
ACCSSIONS B70815
REFERENCE A70500
#authors Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.V.; Eiglmeier, K.; Gas, S.; Barry, T.I.; Chillingworth, T.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holtroyd, S.; Hornsby, T.; Jagels, K.; Krogh, A.; Mclean, J.; Moule, S.; Murphy, L.; Oliver, S.; Osborne, J.; Quail, M.A.;

Rajandream, M.A.; Rogers, J.; Rogers, S.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.; Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

Nature (1998) 393:537-544.

Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.

#cross-references MUID:98295987

#accession B70815

#status preliminary; nucleic acid sequence not shown; translation not shown

#molecule_type DNA

#residues 1-397 ##label COL

#cross-references GB:AL022004; GB:AL123456; NID:g3261550; PID:el254000; PID:g2916917

#experimental_source strain H37Rv

GENETICS

#gene Rv0858c

SUMMARY

#length 397 #molecular-weight 42209 #checksum 1391

Query Match 9.5%; Score 359; DB 2; Length 397;

Best Local Similarity 32.5%; Pred. No. 3.44e-33;

Matches 66; Conservative 51; Mismatches 79; Indels 7; Gaps 7;

Db 44 QRAQDAI-AGVNVQPPGPGSAPLRAIAAQRHFGVDYD-PETEVLVVGVATERIAAA 101

QY 192 DAVAAAVRTGQFCNCPAGVGLPAARSABA-EHLSQ-GVPYMLSAADVFTAGTQIAEVI 249

Db 102 VLGLVE-PGSEVLLIPEFVDSYSPVAMAGAHRTVPLVDPDGRGFDALDARRAVTPRT 160

QY 250 IPVLAGTAGANILLPRGPNYEARAFAFNLEVRHFDLIPD-KGWEIDIDSLESIADKNT 308

Db 161 RALIIINSHPNPTGAVLSATELAAIAEIAVAANLVITDEYIEVFDHARHPLAGFDGM 220

QY 309 TAMVIINPNPCGSVSYDHLKVAEVAEAKRLGILVIADIEVYGLVLSGAPFIPMGVFGHI 368

Db 221 AERTIISSAAKMFNTGKIGW 243

QY 369 T-PVLSTGLSKSKSWIYPGWRLGW 390

RESULT 10

ENTRY aspartate aminotransferase homolog yugH - Bacillus subtilis

TITLE #formal_name Bacillus subtilis

ORGANISM 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change

DATE 24-Sep-1998

G70010

A6580

ACCESSIONS

REFERENCE

#authors

Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertero, M.G.; Bessieres, P.; Bolotin, A.; Borchert, S.; Boriss, R.; Boursier, L.; Brans, A.; Braun, M.; Brignell, S.C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Choi, S.K.; Codani, J.J.; Connerton, I.F.; Cummings, N.J.; Daniel, R.A.; Denizot, F.; Devine, K.M.; Duesterhoef, A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrazi, E.; Foulger, D.; Fritz, C.; Fujita, S.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galleron, N.; Ghim, S.Y.; Glaser, P.; Goffeau, A.; Golightly, E.J.; Grandi, G.; Guisepi, G.; Guy, B.J.; Haga, K.; Halech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.; Itaya, M.; Jones, L.; Joris, B.; Karamata, D.; Kasahara, Y.; Klaerr-Planchard, M.; Klein, C.; Kobayashi, Y.; Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, S.; Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, C.; Medigue, C.; Medina, N.; Mellado, R.P.; Mizuno, M.; Moestl, D.; Nakai, S.; Noback, M.; Noone, D.; O'Reilly, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelie, D.; Porwollik, S.; Prescott, A.M.; Prescan, E.; Pujic, P.; Purnelle, B.; Rapoport, G.; Rey, M.; Reynolds, S.; Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, E.;

Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror, S.J.; Serro, P.; Shin, B.S.; Soldo, B.; Sorokin, A.; Tacconi, E.; Takagi, T.; Takahashi, H.; Takemaru, K.; Takeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, S.; Vandenbol, R.; Vannier, F.; Vassarotti, A.; Viari, A.; Wambutt, R.; Wedler, E.; Wedler, H.; Weitzenegger, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.; Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.

Nature (1997) 390:249-256

The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.

#cross-references MUID:980440033

#accession G70010

#status preliminary; nucleic acid sequence not shown; translation not shown

#molecule_type DNA

#residues 1-357 ##label KUN

#cross-references GB:299120; GB:AL009126; NID:g2635613; PID:el184218; PID:g2635636

#experimental_source strain 168

GENETICS

#gene yugH

CLASSIFICATION

SUMMARY

#length 357 #molecular-weight 39461 #checksum 3672

Query Match 9.5%; Score 355; DB 2; Length 357;

Best Local Similarity 29.3%; Pred. No. 1.35e-32;

Matches 63; Conservative 60; Mismatches 83; Indels 9; Gaps 9;

Db 38 PDFVTANNVREASIIISLQEQ-YTSTANAGLSYSLREETSRYLSNRFDLISYS-PDNEIIVT 95

QY 182 PAFTAVEAEDAAVAARVTGQFCNCPAGVGLPAARSABAHLIS-Q-GVPYMLSAADVFT 239

Db 96 VGASQALDIAIRAIYN-PCGEVVIIPCFVAYDALVSLAGGIPV-HVHTADKGFKATAA 153

QY 240 AGTQIAEVIIPVLAQTAGANILLPRPGYPNFEARAFNR-LEVRHFDLIPKGWEIDID 298

Db 154 DFEAAVTEKIKAILICSPSNPTGVSYSKEELNEIAEFAKKHVDIVLADIIYELIYDEB- 212

QY 299 SLESIADKNTTAMVIINPNPCGSVSYDHLKVAEVAEAKRLGILVIADIEVYGLVLSGAP 358

Db 213 FTSIALPCKMERTVVVISGFSKAFAMTGWRLGFAA 247

QY 359 FIPMGVF-GHITPVLISGLSKSWIYPGWRLGWA 392

RESULT 11

ENTRY H64603 #type complete

TITLE hypothetical protein HP0672 - *Helicobacter pylori* (strain 26695)

ORGANISM #formal_name *Helicobacter pylori*

DATE 30-Jan-1998 #sequence_revision 30-Jan-1998 #text_change

13-Sep-1998

H64603

A64520

ACCESSIONS

REFERENCE

#authors

Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Ketchum, K.A.; Klenk, H.P.; Gill, S.; Dougherty, B.A.; Nelson, K.; Quackenbush, J.; Zhou, L.; Kirkness, E.F.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenney, K.; Fitzgerald, L.M.; Lee, N.; Adams, M.D.; Hickey, E.K.; Berg, D.E.; Gocayne, J.D.; Utterback, T.R.; Peterson, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.; Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.M.; Venter, J.C.

Nature (1997) 388:539-547

The complete genome sequence of the gastric pathogen *Helicobacter pylori*.

#cross-references MUID:97394467

#accession H64603

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##status      preliminary; nucleic acid sequence not shown;
               translation not shown
##molecule_type DNA
##residues    1-390 #label TOM
##cross-references GB:AE000511; TIGR:HP0672
CLASSIFICATION #superfamily aspartate transaminase
SUMMARY        #length 390 #molecular-weight 42874 #checksum 4436

Query Match      9.4%; Score 353; DB 2; Length 390;
Best Local Similarity 25.8%; Pred. No. 2.66e-32;
Matches 93; Conservative 86; Mismatches 163; Indels 19; Gaps 17;

Db 40 PDFTPQAIDAAIKALNDG-FTKYPVAGIPPELLKAIAFKLKKNNLDYEPSEILVNSG 98
QY 182 PAFTAVEAEDAFAAARTGQFNCYPAGVGLPAARSAVAEHLSSQGVPMYLSADDVFLTAG 241
Db 99 AKQSIFNAIQALIE-EGDEVIIPVFWTYPELVKYSQ-GVSQFQTQDEKSHFKTPKQL 156
QY 242 GTQAIEVIVPLVLAQTAGANILLPRGYPNYEARAFNRLEVRHFDLIPDKG-WEIDIDSL 300
Db 157 KDALSPK-TKMLILTPSNPTGMLYSKAELEALGEVLKDKTKVWLSDEIYKLVY-KGEF 214
QY 301 -ESIADKNTTAMVIINPNPCGVSVDHLSKVAEVAERGLGILVIADVEYGLVLSGAPF 359
Db 215 VSCAAVSEMKRTTITIGLSKSVAMTGWGMGYAAASKDKKLVKLMNSLOSQTSINISIT 274
QY 360 IP-MGVFGHIT-PVLSIGLSKSVIWPGRWLGVAVIDPRKILQETKISTITNLYNST 417
Db 275 QMAS-I-VAL-EGLYD-KE--IETMRQAFERCDLAHAKINAIGLN-ALRPDGAFLFI 327
QY 418 DPATFIQAALPOLIENTEDFEKAIIGLLKESSEICYKIKENKYYITCPHKEGSMFVMV 477
Db 328 HTG-SLCG--GDSMRFCHELLEKEGVALVPGKAFGLEGVYVLSFACSEEQIEKGIERTAR 384
QY 478 KLNHLLEEIDDDIDFCCKLAKEESVILCPGSLGMANNWVITFACVPSSLDGLGRIS 537
Db 385 F 385
QY 538 F 538

RESULT 12
ENTRY   H71909 #type complete
TITLE   aspartate aminotransferase - Helicobacter pylori (strain J99)
ORGANISM #formal_name Helicobacter pylori
#variety strain J99
DATE    12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change
        05-Mar-1999
ACCESSIONS H71909
REFERENCE  A71800
#authors   Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.;
           Doig, P.C.; Smith, D.R.; Noonan, B.; Guild, B.C.; deTonge,
           B.L.; Carmel, G.; Tummino, P.J.; Caruso, A.;
           Uria-Nickelsen, M.; Mills, D.M.; Ives, C.; Gibson, R.;
           Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis,
           G.F.; Trust, T.J.
#journal   Nature (1999) 397:176-180
#title     Genomic sequence comparison of two unrelated isolates of the
           human gastric pathogen Helicobacter pylori.
#cross-references MUID:99120557
#accession H71909
#status    preliminary
#molecule_type DNA
#residues  1-390 #label ARN
##cross-references GB:AE001493; GB:AE001439; NID:g4155161; PID:g4155168
##experimental_source strain J99

GENETICS
#gene      aspB
#superfamily aspartate transaminase
CLASSIFICATION #length 390 #molecular-weight 42746 #checksum 4845
SUMMARY

Query Match      9.3%; Score 349; DB 2; Length 390;
Best Local Similarity 25.8%; Pred. No. 1.04e-31;

Db 42 PDFNTQIMDAADSMOOG-YTKYTPSGGLPALKOATIEKFRDNQLEKPNELIIVGVG 100
QY 182 PAFTAVEAEDAFAAARTGQFNCYPAGVGLPAARSAVAEHLSSQGVPMYLSADDVFLTAG 241
Db 101 AKHVLTYLTFQVILN-EGDEVIIPIYVWYTPQYKLAG-GVPVYIATSEQNYKITAEQL 158
QY 242 GTQAIEVIVPLVLAQTAGANILLPRGYPNYEARAFNRLEVRHF-DLIPDKGWEIDIDSL 300
Db 159 KNAITDK-TRAVIINSPNPTGMVYTRREEEDIAKIALENNILVSDIYEPKLYNGAEH 217
QY 301 -ESIADKNTTAMVIINPNPCGVSVDHLSKVAEVAERGLGILVIADVEYGLVLSGAPF 359
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Matches 93; Conservative 84; Mismatches 165; Indels 19; Gaps 17;

Db 40 PDFTPQAIDAAIKALNDG-FTKYPVAGIPPELLKAIAFKLKKNNLDYEPSEILVNSG 98
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Db 99 AKQSIFNAIQALIE-EGDEVIIPVFWTYPELVKYSQ-GVSQFQTQDEKSHFKTPKQL 156
QY 242 GTQAIEVIVPLVLAQTAGANILLPRGYPNYEARAFNRLEVRHFDLIPDKG-WEIDIDSL 300
Db 157 KDALSPK-TKMLILTPSNPTGMLYSKAELEALGEVLKDKTKVWLSDEIYKLVY-KGEF 214
QY 301 -ESIADKNTTAMVIINPNPCGVSVDHLSKVAEVAERGLGILVIADVEYGLVLSGAPF 359
Db 215 VSCAAVSEMKRTTITIGLSKSVAMTGWGMGYAAASKDKKLVKLMNSLOSQTSINISIT 274
QY 360 IP-MGVFGHIT-PVLSIGLSKSVIWPGRWLGVAVIDPRKILQETKISTITNLYNST 417
Db 275 QMAS-I-VAL-EGLYD-KE--IETMRQAFERCDLAHAKINAIGLN-ALRPDGAFLFI 327
QY 418 DPATFIQAALPOLIENTEDFEKAIIGLLKESSEICYKIKENKYYITCPHKEGSMFVMV 477
Db 328 HTG-SLCG--GDSMRFCHELLEKEGVALVPGKAFGLEGVYVLSFACSEEQIEKGIERTAR 384
QY 478 KLNHLLEEIDDDIDFCCKLAKEESVILCPGSLGMANNWVITFACVPSSLDGLGRIS 537
Db 385 F 385
QY 538 F 538

RESULT 13
ENTRY   A38621 #type complete
TITLE   aspartate transaminase [EC 2.6.1.1] - Bacillus sp. (strain
        YM-2)
ALTERNATE_NAMES aspartate aminotransferase
ORGANISM         #formal_name Bacillus sp.
DATE            23-Aug-1991 #sequence_revision 23-Aug-1991 #text_change
        13-Sep-1998
ACCESSIONS A38621
REFERENCE  A38621
#authors   Sung, M.H.; Tanizawa, K.; Tanaka, H.; Kuramitsu, S.;
           Kagamiyama, H.; Hirotsu, K.; Okamoto, A.; Higuchi, T.;
           Soda, K.
#journal   J. Biol. Chem. (1991) 266:2567-2572
#title     Thermostable aspartate aminotransferase from a thermophilic
           Bacillus species. Gene cloning, sequence determination, and
           preliminary X-ray characterization.
#cross-references MUID:91115885
#accession A38621
#status    preliminary
#molecule_type DNA
#residues  1-392 #label SUN
##cross-references GB:M59430; NID:g142537; PID:g142538
CLASSIFICATION #superfamily aspartate transaminase
KEYWORDS       aminotransferase
SUMMARY        #length 392 #molecular-weight 42661 #checksum 7039

Query Match      9.2%; Score 344; DB 2; Length 392;
Best Local Similarity 23.7%; Pred. No. 5.65e-31;
Matches 86; Conservative 103; Mismatches 154; Indels 20; Gaps 18;

Db 42 PDFNTQIMDAADSMOOG-YTKYTPSGGLPALKOATIEKFRDNQLEKPNELIIVGVG 100
QY 182 PAFTAVEAEDAFAAARTGQFNCYPAGVGLPAARSAVAEHLSSQGVPMYLSADDVFLTAG 241
Db 101 AKHVLTYLTFQVILN-EGDEVIIPIYVWYTPQYKLAG-GVPVYIATSEQNYKITAEQL 158
QY 242 GTQAIEVIVPLVLAQTAGANILLPRGYPNYEARAFNRLEVRHF-DLIPDKGWEIDIDSL 300
Db 159 KNAITDK-TRAVIINSPNPTGMVYTRREEEDIAKIALENNILVSDIYEPKLYNGAEH 217
QY 301 -ESIADKNTTAMVIINPNPCGVSVDHLSKVAEVAERGLGILVIADVEYGLVLSGAPF 359
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Db	218	FSIAQLSEVKAQTIVINCYSKSHSWTGRIGYANG-NADLIINAMTDLASHSTSNPTAS	276
QY	359	FIPMGVFGHI-TFVLSIGLSKSWTPVGRWGVAVYDPKRILQETKISTINYLNVST	417
Db	277	OYAAIEAYNGPO-DSV-EEMKSAFESRL-ET-T-YPKLSAIPGFKV-KPOGAFVLLP	328
QY	418	DPATFIQAALPOLIENTWEDFFKAIIGLLKSSSELCYQIKENKYITCPHKPEGSMFVW	477
Db	329	DVS-EAAQKTGFASVDEFASALLTEANVAVIPGSGFAGPASTIRISYATSLNLEAEARI	387
QY	478	KLNLHLEIID-DDID-FOCKLAKEESVILCPGSLGVLMANWVRITFACVPSSLQDLGRI	535
Db	388	DRF 390	
QY	536	KSF 538	
RESULT ENTRY TITLE	14	A69516 #type complete aspartate aminotransferase (aspB-2) homolog - Archaeoglobus fulgidus	
ORGANISM		#formal_name Archaeoglobus fulgidus	
DATE		05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 13-Sep-1998	
ACCESSIONS		A69516	
REFERENCE		A69250	
authors		Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson, R.J.; Gwinn, M.; Hickey, E.K.; Peterson, J.D.; Richardson, D.L.; Kerlavage, A.R.; Graham, D.E.; Kyripides, N.C.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.; Dougherty, B.A.; McKenry, K.; Adams, M.D.; Loftus, B.; Peterson, S.; Reich, C.I.; McNeil, L.K.; Badger, J.H.; Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.; Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.M.; Sadow, P.W.; D'Andrea, K.P.; Bowman, C.; Fujii, C.; Garland, S.A.; Mason, T.M.; Olsen, G.J.; Fraser, C.M.; Smith, H.O.; Woese, C.R.; Venter, J.C.	
#journal		Nature (1997) 390:364-370	
#title		The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeon Archaeoglobus fulgidus.	
#cross-references		MUID:98049343	
#accession		A69516	
#status		preliminary; nucleic acid sequence not shown; translation not shown	
#molecule_type		DNA	
#residues		1-379 #label KLE	
#cross-references		GB:AE000957; GB:AE000782; NID:g2689280; PID:g2648397;	
CLASSIFICATION SUMMARY		#superfamily aspartate transaminase #length 379 #molecular-weight 42699 #checksum 2429	
Query Match		8.6%; Score 323; DB 2: Length 379;	
Best Local Similarity		26.4%; Pred. No. 6,71e-28;	
Matches		95; Conservative 95; Mismatches 143; Indels 27; Gaps 20;	
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QY	182	PAFTAVEADAARAAVRTQFCNYPAGVGLPAARSAVAEHLSSQGPYMLSDADDVFLTAG	241
Db	101	AKVAIFAMCILL-QSGDEVILLD-PSWYSYEA-CIL-MAGAKPVWVHEEGFE-D-API	154
QY	242	GTQAI-EVILPVLAQTAGANILLPRGYPNYEARAFNLEVRHFDLPIDKGWEIDIDL	300
Db	155	EDYITSNTKMIIVTSPNLGVVPEFLKKRDLAVDRKDLVMSDEIYEIKIIEGEHYS	214
QY	301	ESTADKNTTAMVINPNPCGSVSYDHLKSAEVAKRGLIVIADEVYGLVLGSAPFI	360
Db	215	LAAMGMLERTITINGFSKTSYMTGNRLGVAAPE-W-II---KLMNRQSH-SVS-HPT	267
QY	361	PMGVFGHITPVLSTGLSKSWIPVGRWGVAVYDPKRILQETKISTINYLNVSTOPA	420

[illegible][illegible]

Fri Oct 1 16:47:09 1999

US-09-026-400-4.rpr

Page 9

QY 533 GRI 535

Search completed: Fri Oct 1 13:55:46 1999
Job time : 32 secs.

(TM)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Oct 1 13:53:33 1999; MasPar time 17.07 Seconds
912.281 Million cell updates/sec
Tabular output not generated.

Title: >US-09-026-400-4
Description: (1-551) from US09026400.pep
Perfect Score: 3749
Sequence: 1 MATVRQSDGVAANGLAVAAA.....LGRKSFQCRNKRNSDDC 551

Scoring table: PAM 150
Gap 11

Searched: 77977 seqs, 28268293 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot37
1:swissprot

Statistics: Mean 51.972; Variance 111.846; scale 0.465

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	952	25.4	454	1	ATTY_RAT	
2	921	24.6	454	1	TYROSINE AMINOTRANSFER	2.68e-149
3	586	15.6	416	1	ATTY_TRYCR	2.25e-143
4	374	10.0	401	1	AAT_SULSO	2.66e-80
5	370	9.9	375	1	ASPARTATE AMINOTRANSF	5.21e-42
6	344	9.2	392	1	PUTATIVE ASPARTATE AMI	2.61e-41
7	336	9.0	393	1	ASPARTATE AMINOTRANSF	8.03e-37
8	319	8.5	393	1	ASPARTATE AMINOTRANSF	2.07e-35
9	304	8.1	392	1	PUTATIVE AMINOTRANSF	1.69e-32
10	287	7.7	400	1	PUTATIVE AMINOTRANSF	5.95e-30
11	288	7.7	507	1	PUTATIVE ALANINE AMINO	4.29e-27
12	289	7.7	592	1	PUTATIVE ALANINE AMINO	2.92e-27
13	253	6.7	444	1	YJGO_YEAST	1.98e-27
14	251	6.7	505	1	PUTATIVE ALANINE AMINO	1.73e-21
15	247	6.6	410	1	ALAT_SCHPO	3.65e-21
16	244	6.5	421	1	ASPARTATE AMINOTRANSF	1.62e-20
17	240	6.4	386	1	YBDL_ECOLI	4.94e-20
18	230	6.1	482	1	HYPOTHETICAL AMINOTRAN	2.17e-19
19	229	6.1	517	1	ALANINE AMINOTRANSFER	8.54e-18
20	219	5.8	399	1	1A1C_DIACA	1.23e-17
21	218	5.8	482	1	PROBABLE ASPARTATE AMI	1.23e-17
22	212	5.7	412	1	ALANINE AMINOTRANSFER	4.62e-16
23	202	5.4	213	1	YFDZ_ECOLI	6.62e-15
					HYPOTHETICAL AMINOTRAN	5.68e-15
					PROBABLE ASPARTATE AMI	1.97e-13

24	202	5.4	387	1	PATB_BACSU	PUTATIVE AMINOTRANSFER	1.97e-13
25	194	5.2	418	1	YD91_METJA	PUTATIVE AMINOTRANSFER	3.22e-12
26	196	5.2	493	1	1A11_CUCMA	1-AMINOCYCLOPROPANE-1-	1.60e-12
27	193	5.1	361	1	HIS8_HALVO	HISTIDINOL-PHOSPHATE A	4.55e-12
28	190	5.1	393	1	CSP_PLABR	CIRCUMSPOROZOITE PROTE	1.28e-11
29	182	5.1	475	1	1A12_CUCMA	1-AMINOCYCLOPROPANE-1-	6.43e-12
30	188	5.0	429	1	CSP_PLAMA	CIRCUMSPOROZOITE PROTE	2.55e-11
31	187	5.0	495	1	ALAT_RAT	ALANINE AMINOTRANSFER	3.60e-11
32	184	4.9	347	1	MSA2_PLAF2	MEROZOITE SURFACE ANTI	1.00e-10
33	184	4.9	385	1	HIS8_YEAST	HISTIDINOL-PHOSPHATE A	1.00e-10
34	183	4.9	419	1	CSP_PLACM	CIRCUMSPOROZOITE PROTE	1.41e-10
35	185	4.9	493	1	1A11_CUCPE	1-AMINOCYCLOPROPANE-1-	7.13e-11
36	180	4.8	390	1	MALY_ECOLI	MALY PROTEIN (EC 2.6.1	3.90e-10
37	181	4.8	470	1	YJIR_ECOLI	HYPOTHETICAL 53.0 KD P	2.78e-10
38	178	4.7	376	1	HIS8_SULSO	HISTIDINOL-PHOSPHATE A	7.65e-10
39	177	4.7	494	1	1A12_CUCPE	1-AMINOCYCLOPROPANE-1-	1.07e-09
40	174	4.6	219	1	HIS8_MYCSM	HISTIDINOL-PHOSPHATE A	2.93e-09
41	174	4.6	398	1	CSP_PLACC	CIRCUMSPOROZOITE PROTE	2.93e-09
42	174	4.6	476	1	1A14_LYCFS	1-AMINOCYCLOPROPANE-1-	2.93e-09
43	172	4.6	495	1	ALAT_HUMAN	ALANINE AMINOTRANSFER	5.70e-09
44	168	4.5	401	1	CSP_PLACG	CIRCUMSPOROZOITE PROTE	2.14e-08
45	165	4.4	384	1	HIS8_SCHPO	HISTIDINOL-PHOSPHATE A	5.72e-08

ALIGNMENTS

RESULT 1
ID ATTY_RAT STANDARD; PRT; 454 AA.
AC P04694;
DT 13-AUG-1987 (REL. 05, CREATED)
DT 13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE TYROSINE AMINOTRANSFERASE (EC 2.6.1.5) (L-TYROSINE:2-OXOGLUTARATE AMINOTRANSFERASE) (TAT).
GN TAT.
OS RATTUS NORVEGICUS (RAT).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; RATTUS.
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 85293103.
RA GRANGE T., GUNET C., DIETRICH J.-B., CHASSEROT S., FROMONT M., BEFORT N., JAMI J., BECK G., PICTET R.;
RT "Complete complementary DNA of rat tyrosine aminotransferase messenger RNA. Deduction of the primary structure of the enzyme.";
RL J. MOL. BIOL. 184:347-350(1985).
[2]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE; 89079691.
RA HARGROVE J.L., SCOBLE H.A., MATHEWS W.R., BAUMSTARK B.R., BIEMANN K.;
RT "The structure of tyrosine aminotransferase. Evidence for domains involved in catalysis and enzyme turnover.";
RL J. BIOL. CHEM. 264:45-53(1989).
[3]
RP SEQUENCE OF 190-386 FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE; 92190544.
RA MOROZOV I.V.;
RT "Nucleotide sequence of rat liver tyrosine aminotransferase gene fragment.";
RL DNA SEQ. 1:151-155(1990).
[4]
RP PARTIAL SEQUENCE.
RX MEDLINE; 92038067.
RA LORBER B., DIETRICH J.-B., KERN D.;
RT "Isolation and characterization of active N-terminal truncated apo- and holoenzyme of mammalian liver tyrosine aminotransferase.";
RL FEBS LETT. 291:345-349(1991).
[5]
RP STRUCTURAL PROPERTIES.
RX MEDLINE; 89000971.
RA DIETRICH J.-B., GENOT G., BECK G.;

Fri Oct 1 16:47:09 1999

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RC STRAIN=ATCC 49255 / MT4;
RX MEDLINE: 94298815;
RA ZAPPACOSTA F., SANNIA G., SAVOY L.A., MARINO G., PUCCI P.;
RT "Post-translational modifications in aspartate aminotransferase from
RT Sulfolobus solfataricus. Detection of N-epsilon-methyllysines by mass
RT spectrometry."
RL EUR. J. BIOCHEM. 222:761-767(1994).
RN [3]
RP SEQUENCE OF 1-22;
RC STRAIN=ATCC 49255 / MT4;
RX MEDLINE: 88315018;
RA MARINO G., NITTI G., ARNONE M.I., SANNIA G., GAMBACORTA A.,
RA DE ROSA M.;
RT "Purification and characterization of aspartate aminotransferase from
RT the thermocidophilic archaeobacterium Sulfolobus solfataricus.";
RL J. BIOL. CHEM. 263:12305-12309(1988).
RN [4]
RP SEQUENCE OF 239-250;
RC STRAIN=ATCC 49255 / MT4;
RX MEDLINE: 92062695;
RA BIRLOLO L., ARNONE M.I., CUBELLIS M.V., ANDREOTTI G., NITTI G.,
RA MARINO G., SANNIA G.;
RT "The active site of Sulfolobus solfataricus aspartate
RT aminotransferase."
RL BIOCHIM. BIOPHYS. ACTA 1080:198-204(1991).
CC -!- CATALYTIC ACTIVITY: L-ASPARTATE + 2-OXOGLUTARATE = OXALOACETATE +
CC L-GLUTAMATE.
CC -!- COFACTOR: PYRIDOXAL PHOSPHATE.
CC -!- SUBUNIT: HOMODIMER.
CC -!- THIS ENZYME OPTIMUM TEMPERATURE IS ABOVE 95 DEGREES CELSIUS.
CC -!- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT
CC AMINOTRANSFERASES.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X16505; G809765; -
CC PIR: S07088; S07088.
CC PIR: S18362; S18362.
CC PIR: S21189; S21189.
CC PROSITE: PS00105; AA_TRANSFER_CLASS_1; 1.
CC PFAM: PF00155; aminotran_1; 1.
CC TRANSFERASE; AMINOTRANSFERASE; PYRIDOXAL PHOSPHATE; METHYLATION.
CC INIT_MET 0
CC BINDING 241 241 PYRIDOXAL PHOSPHATE.
CC MOD_RES 202 202 METHYLATION (MONO-) (PARTIAL).
CC MOD_RES 384 384 METHYLATION (MONO-) (PARTIAL).
CC SEQUENCE 401 AA; 45600 MW; DF51D490 CRC32;
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Matches 92; Conservative 122; Mismatches 152; Indels 24; Gaps 20;
Db 21 YKEARNVEKTKIKIIDFGIGQDPL-PTFKR-IR--DAAKEALDQG-FTFTYGAQIDE 75
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| | | | : : : : | | | | : : : : | | | | : : : : |
156 YK-ISASVQEGRPVLPPLAHGDPVSVEFAERTAVEADAFAVAVRTGQFCYPAAGVGLPA 214
| | | | : : : : | | | | : : : : | | | | : : : : |
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76 LREKIAQLNTRYGDVYKKEVITVPKAPALFLVF-ILYNPSDEVILLPPSYSAEV 134
| | | | : : : : | | | | : : : : | | | | : : : : |
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215 ARSAVEHLNSQGVPMYLSADDFVTAGTQAEIVLPIVLAQTAGANILLPRGYPNY-EA 273
| | | | : : : : | | | | : : : : | | | | : : : : |
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135 VKLLGGKPIYANLWKSREGEFSIDVDDLSQSKISRTKMKIVFNPNHNPFTGLFSPNDVKKI 194
| | | | : : : : | | | | : : : : | | | | : : : : |
| | | | : : : : | | | | : : : : | | | | : : : : |
274 -RAAFNRLEVRHFDLIPKQWEIDIDSLESIAADKNTTAMVINPNPCGSVSYVDHLSKV 332
| | | | : : : : | | | | : : : : | | | | : : : : |
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195 VDISRDNKIILSDIEYDNFVYEGKMRSTLEDSWDRLIIVNGFSFTKFTWGRGLYI- 253
| | | | : : : : | | | | : : : : | | | | : : : : |
| | | | : : : : | | | | : : : : | | | | : : : : |
333 AEVAKRLGILVIADEVYGLKGLSAPFIPMGVFGHITPVLISGLSKSWIYPPGWRGLGWA 392
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Db 254 V-AKREIIQ--KMGI-LAA--NVVTAPTSTFYQAAKAFD-TFDEV-NQMYSLFKKRDV 305
| | | | : : : : | | | | : : : : | | | | : : : : |
| | | | : : : : | | | | : : : : | | | | : : : : |
QY 393 VYDPRKILQETKISTITNYLNVSDPATFIOAALPQLENTKEDFFKRAIIGLLKESSEI 452
| | | | : : : : | | | | : : : : | | | | : : : : |
| | | | : : : : | | | | : : : : | | | | : : : : |
Db 306 MYDELTKVKGVEVS-KPNGAFYMPNVS-KILTKSGFDVKSIAIKIEKGWVPIPGEVF 363
| | | | : : : : | | | | : : : : | | | | : : : : |
| | | | : : : : | | | | : : : : | | | | : : : : |
QY 453 CYQIKENKYITCPHKPEGSFVWVKLNHLLEEDDDI-DFCCKLAKEESVILCPGSV- 510
| | | | : : : : | | | | : : : : | | | | : : : : |
| | | | : : : : | | | | : : : : | | | | : : : : |
Db 364 PLNIGKEFLRLSFAVNEEVIREQIKREF 393
| | | | : : : : | | | | : : : : | | | | : : : : |
| | | | : : : : | | | | : : : : | | | | : : : : |
QY 511 -LGMAN-WRITFACVPSSLODGLGRKSF 538
| | | | : : : : | | | | : : : : | | | | : : : : |
| | | | : : : : | | | | : : : : | | | | : : : : |
RESULT 5
ID AA11_METJA STANDARD; PRT; 375 AA.
AC Q60317;
DT 01-NOV-1997 (REL. 35, CREATED)
DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE PUTATIVE ASPARTATE AMINOTRANSFERASE 1 (EC 2.6.1.1) (TRANSAMINASE A)
DE (ASPART).
GN MJ0001.
OS METHANOCOCCUS JANNASCHII.
OC ARCHAEA: EURYARCHAEOTA; METHANOCOCCALES; METHANOCOCCACEAE;
OC METHANOCOCCUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE: 96337999;
RA BULT C.J., WHITE O., OLSEN G.J., ZHOU L., FLEISCHMANN R.D.,
RA SUTTON G.G., BLAKE J.A., FITZGERALD L.F., ADAMS M.D., REICH C.I.,
RA KERRAVAGE A.R., DOUGHERTY B.A., TOMB J.-F., MERRICK J.M., GLODEK A.,
RA OVERBECK R., KIRKNESS E.F., WEINSTOCK K.G., FUHRMANN J.L., NGUYEN D.,
RA SCOTT J.L., GOGHAGEN N.S.M., WEIDMAN J.D., SADOW P.W., HANNA M.C.,
RA UTTERBACK T.R., KELLEY J.M., PETERSON J.D., BURTON M.A., KOTTON M.D., ROBERTS K.M., HURST M.A., RAINE B.P., BORODOVSKY M.,
RA KLENK H.-P., FRASER C.M., SMITH H.O., WOESE C.R., VENTER J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
RT jannaschii."
RL SCIENCE 273:1058-1073(1996).
CC -!- CATALYTIC ACTIVITY: L-ASPARTATE + 2-OXOGLUTARATE = OXALOACETATE +
CC L-GLUTAMATE (BY SIMILARITY).
CC -!- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT
CC AMINOTRANSFERASES.
CC -----
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CC -----
CC EMBL: U67459; G1592252; -
CC TIGR: MJ0001; -
CC PROSITE: PS00105; AA_TRANSFER_CLASS_1; 1.
CC PFAM: PF00155; aminotran_1; 1.
CC TRANSFERASE; AMINOTRANSFERASE; PYRIDOXAL PHOSPHATE.
CC BINDING 223 223 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
CC SEQUENCE 375 AA; 42395 MW; 166A9EFC CRC32;
CC -----
Query Match 9.9%; Score 370; DB 1; Length 375;
Best Local Similarity 26.9%; Pred. No. 2, 61e-41;
Matches 97; Conservative 100; Mismatches 136; Indels 28; Gaps 26;
Db 33 PDFDTPKHIIIEAKRALDEKTH-YSPNNGIPELREISNKLDDYNDVDKNIIYTCG 91
| | | | : : : : | | | | : : : : | | | | : : : : |
| | | | : : : : | | | | : : : : | | | | : : : : |
QY 182 PAFRTAVEADAFAVAVRTGQFCYPAAGVGLPAARSVAEHLNSQGVPMYLSADDFVTAG 241
| | | | : : : : | | | | : : : : | | | | : : : : |
| | | | : : : : | | | | : : : : | | | | : : : : |
Db 92 ASEALMSIMTLIDR-GDEVLPNPSFVSFSLTEFAEGKIKIDL--DENFNIDLEKVK 148
| | | | : : : : | | | | : : : : | | | | : : : : |
| | | | : : : : | | | | : : : : | | | | : : : : |

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QY 242 GTOAEVITPVLAQTAGANILLPRGYPNYEARAFNRLEVRHFDLIPDKGWEIDIDS1- 300
Db 149 ESIT-KTKLIIFSPNSPTGKVVDEKTIKGLAEIAEDYNLIIVSDENVYDKKIYKKHVS 207
QY 301 ESIADKNTAMVINPNPCGSVSYDHLKVAEAKRGLIVIADEVYKVLVSAPFI 360
Db 208 PMQ-FTD-RCIL-INGFSKTYAMTGWIRIGYLAVSDLNKELDLINNMIKIHOY-SFAC-A 262
QY 361 PMGVFGHTPVLSIGLSKSWIVPGWRLGWAVYDP-RKILQETKISTITINLVSTDP 419
Db 263 TTEAQYGAAL-GRGS-OKCVEDMREFKMRDLINGLKD1-FKV--NKPDGA-FY-I- 314
QY 420 AIFIQ-AALPOLIENTEDFFKALIGLKSSEICYKQIKENKYYTCPCPKPGSMFVWK 478
Db 315 FP-DV-SEYGVGEVAKKLI-ENKV-LCPVGFAGENGANGYIRFSYATYEDIERKALGII 370
QY 479 LNLHLEEDIDDFCKLAKESVILC-PGSVLG-M-ANWVRITFACVPSSLQDGLGRI 535
Db 371 K 371
QY 536 K 536

RESULT 6
ID AAT_BACSP STANDARD; PRT; 392 AA.
AC 223034; 1991 (REL. 20, CREATED)
DT 01-NOV-1991 (REL. 20, LAST SEQUENCE UPDATE)
DT 01-NOV-1991 (REL. 34, LAST ANNOTATION UPDATE)
DE ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1) (TRANSAMINASE A) (ASPART).
OS BACILLUS SP. (STRAIN YM-2).
OC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
OC BACILLUS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 91115885.
RA SUNG M.H., TANIZAWA K., TANAKA H., KURAMITSU S., KAGAMIYAMA H.,
RA HIROTSU K., OKAMOTO A., HIGUCHI T., SODA K.;
RT "Thermostable aspartate aminotransferase from a thermophilic Bacillus
RT species. Gene cloning, sequence determination, and preliminary X-ray
RT characterization.";
RJ J. BIOL. CHEM. 266:2567-2572(1991).
RN [2]
RP SEQUENCE OF 1-24 AND 387-392.
RX MEDLINE; 90170846.
RA SUNG M.H., TANIZAWA K., TANAKA H., KURAMITSU S., KAGAMIYAMA H.,
RA SODA K.;
RT "Purification and characterization of thermostable aspartate
RT aminotransferase from a thermophilic Bacillus species.";
RJ J. BACTERIOL. 172:1345-1351(1990).
CC -!- CATALYTIC ACTIVITY: L-ASPARTATE + 2-OXOGLUTARATE = OXALACETATE +
CC L-GLUTAMATE.
CC -!- COFACTOR: PYRIDOXAL PHOSPHATE.
CC -!- SUBUNIT: HOMODIMER.
CC -!- THIS THERMOSTABLE ENZYME IS MOST ACTIVE AT 70 DEGREES CELSIUS.
CC -!- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT
CC AMINOTRANSFERASES.
CC -----
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CC -----
DR EMBL; M59430; G142538; .
DR PIR; A38621; A38621
DR PROSITE; PS00105; AA_TRANSFER_CLASS_1; 1.
DR PFAM; PF00155; aminotran_1; 1.
KW TRANSFERASE; AMINOTRANSFERASE; PYRIDOXAL PHOSPHATE.
FT BINDING 239 239 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
FT CONFLICT 388 388 D -> L (IN REF. 2).
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SQ SEQUENCE 392 AA; 42661 MW; 8FOEC6D0 CRC32;
Query Match 9.2%; Score 344; DB 1; Length 392;
Best Local Similarity 23.7%; Pred. No. 8.63e-37;
Matches 86; Conservative 103; Mismatches 154; Indels 20; Gaps 18;

Db 42 PDNTONTIMDAIDSMMQOG-YTKYTPSGGLPALKQAIIEKFRDNQLEYKPNIEIVGV 100
QY 182 PAFRTAVEADEAATAVARTQCFNCYPAGVGLPAARSVAEHLSCQVPYMLSADDVFLTAG 241
Db 101 AKHVLATLFOVILN-BGDEVILPIPVWSYSPQVLAG-GVPVYIETATSEQNYKITAOL 158
QY 242 GTOAEVITPVLAQTAGANILLPRGYPNYEARAFNRLEVRHFDLIPDKGWEIDIDS1 300
Db 159 KNAITDK-KTAVIINSNPSTGMVYTRREELEDAKALENNILIVSDIYEKLYNGAEH 217
QY 301 -ESIAKNTTAMVIINPNPCGSVSYDHLKVAEAKRGLIVIADEVYKVLV-GSAP 358
Db 218 FSTAQISEEVKAQTIINGVSKSHSMTGHRIGYAG-NADIINAMTDLASHSTSNPTTAS 276
QY 359 FIPMGVFGHI-TPVLSIGLSKSWIVPGWRLGWAVYDPKILQETKISTITINLVST 417
Db 277 QYAAIEAYNGPQ--DSV-BEMRKAFESRL-ET--I-YPKLSAIPGFKVY-KPGQAFYLLP 328
QY 418 DPATFIOAALPOLIENTEDFFKALIGLKSSEICYKQIKENKYYTCPCPKPGSMFVWK 477
Db 329 DVS-EAAQKTGFASVDFEASALLTEANVAVIPGSGFAGPSTIRISYATSLNIEAERI 387
QY 478 KLNHLLEEID-DDID-FCKLAKESVILCPSVLGMANWVRITFACVPSSLQDGLGRI 535
Db 388 DRF 390
QY 536 KSP 538

RESULT 7
ID AAT_BACST STANDARD; PRT; 393 AA.
AC Q59228;
DT 01-NOV-1997 (REL. 35, CREATED)
DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1) (TRANSAMINASE A) (ASPART).
GN ASPC.
OS BACILLUS STEAROTHERMOPHILUS.
OC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
OC BACILLUS.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-ATCC 12980;
RX MEDLINE; 96434469.
RA BARTSCH K., SCHNEIDER R., SCHULZ A.;
RT "Stereospecific production of the herbicide phosphinothricin
RT (glufosinate): purification of aspartate transaminase from Bacillus
RT stearothermophilus, cloning of the corresponding gene, aspcC, and
RT application in a coupled transaminase process.";
RJ APPL. ENVIRON. MICROBIOL. 62:3794-3799(1996).
CC -!- CATALYTIC ACTIVITY: L-ASPARTATE + 2-OXOGLUTARATE = OXALACETATE +
CC L-GLUTAMATE.
CC -!- COFACTOR: PYRIDOXAL PHOSPHATE.
CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT
CC AMINOTRANSFERASES.
CC -----
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DR EMBL; X93600; E212847; .
DR PROSITE; PS00105; AA_TRANSFER_CLASS_1; 1.
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Fri Oct 1 16:47:09 1999

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DR PFAM: PF00155; aminotran_1; 1.
KW TRANSFERASE; AMINOTRANSFERASE; PYRIDOXAL PHOSPHATE.
FT BINDING 237 237 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
SQ SEQUENCE 393 AA; 42401 MW; 64949162 CRC32;

Query Match 9.0%; Score 336; DB 1; Length 393;
Best Local Similarity 23.88; Pred. No. 2,07e-35;
Matches 86; Conservative 102; Mismatches 156; Indels 18; Gaps 17;

Db 40 PDFTFQHIILDAAIKAMNEGHTKYTPSG-GLFALKEEIIKKFARDQGLDYEPAAVIVCVG 98
QY 182 PAFRTAVEAEDAAAVARTQGFNCYPAGVGLPAARSAVAEHLISQGVPMLSADDFELTAG 241
Db 99 AKUALYTLFOVLDD-EGDEVIIPTPWVSYPEQVKLAG-GVPYVYEGLEQNHFKITPEOL 156
QY 242 GTOAIEVYIIPVLAQTAGANTLLPRPGYPNYEARAAFNRLVHRF-DLIIDPKGWEIDISL 300
Db 157 KOAITPR-TRAVIINSPSNPTGIYTAEEELKALGEVCLAHGLVIVSDEIYEIKLTYGGAKH 215
QY 301 -ESIADKNITAMVLIINPNPCGVSYSVDHLSKVAEYAKRGLILVIADEVYGLVLSGAPF 359
Db 216 VSTAELSPKLAQTVIINGYSKSHMTGWRIGYAA--GPRDIK-A-M-TDLASH-STS- 268
QY 360 IPMGVFG-HI-TPVLSIGSLSKSWIPVGRWLVAVDPKRIQETKISTITNVLNVST 417
Db 269 NPSTIAQYAAIAYSQGPQEPV-FQMRQAPFQRLNIYDKLVQIPGFTCV-KQGAFFYLP 326
QY 418 DPATFIQAALPQILENTKEDFFKRAITGLLKESSEICYKQIKENKYITICPHKPGSMFVMV 477
Db 327 NAREAAAAMAGRTVDEFFVAALLBEAKVALVPGFGFAGPNDVRSYATSLDALETAYERIH 386
QY 478 KL-NHLLEEIDDDIDFCCKLAKAESVILCPGSLGMANWVRITACVPSSLQDGLGRIK 536
Db 387 RF 388
QY 537 SF 538

RESULT 8
ID AATL_BACSU STANDARD; PRT; 393 AA.
AC P33001;
RC 01-OCT-1996 (REL. 34, CREATED)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DE 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
DE ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1) (TRANSAMINASE A) (ASPART.
GN ASPF.
OS BACILLUS SUBTILIS.
OC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
RN BACILLUS.
RC [1]
RC SEQUENCE FROM N.A.
RC STRAIN-168 / MAREBURG;
RX MEDLINE; 96349105.
RA SOROKIN A.V., ALEVEDO V., ZUMSTEIN E., GALLERON N., EHRlich S.D.,
RA ERROR P.;
RT "Sequence analysis of the Bacillus subtilis chromosome region between
RT the serA and kds loci cloned in a yeast artificial chromosome." ;
RL MICROBIOLOGY 142:2005-2016(1996).
CC -!- CATALYTIC ACTIVITY: L-ASPARTATE + 2-OXOGLUTARATE = OXALOACETATE +
CC L-GLUTAMATE.
CC -!- COFACTOR: PYRIDOXAL PHOSPHATE.
CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT
CC AMINOTRANSFERASES.
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DR EMBL; L47709; G1146246; -.
DR EMBL; Z99115; E1183682; -.
DR SUBTILIST; BG11513; ASPB.
DR PROSITE; P800105; AA_TRANSFERR_CLASS_1; 1.
DR PFAM; PF00155; aminotran_1; 1.
KW TRANSFERASE; AMINOTRANSFERASE; PYRIDOXAL PHOSPHATE.
FT BINDING 237 237 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
SQ SEQUENCE 393 AA; 43088 MW; 930F37D6 CRC32;

Query Match      8.5%; Score 319; DB 1; Length 393;
Best Local Similarity 22.7%; Pred.No.1.69e-32;
Matches      83; Conservative 111; Mismatches 155; Indels 16; Gaps 15;

Db    40 PDNTPQHIIIDAAVRSNMNEGHKTYTPSG-GLAELKNSIAEKEFKRDQNIKYKPQSIIVCTG 98
      | | | : : : | : : | : : | : : | : : | : : | : : | : : | : : | : : |
Qy    182 PAFTAFAVEDAVAAAVRTQFCYCPAGVGLPAARGAUAHLSQGVPYMLSADDFVLTAG 241
      | | | : : : | : : | : : | : : | : : | : : | : : | : : | : : | : : |
Db    99 AKHALYTLFWILD-EDEVEIITPTWVSYPEQVKLAGGPVVVEGLEENHFHKISPEQLK 157
      k h l y t l f w i l d - e d e v e i i p t w v s y p e q v k l a g g p v v e g l e e n h f h k i s p e q l k
Qy    242 GTQAIEVIIPVLAQTAGANILLPRPGYPNPYEARAARNREVRHFDLPDRKGWEIDDSL- 300
      g t q a i e v i i p v l a q t a g a n i l l p r p g y p n p y e a r a a r n r e v r h f d l p d r k g w e i d d s l -
Db    158 NAITEK-TKAIVNSPNPFGVMKTEELSALGEVCLEHDILLVSEIYEKLAYGGKKHV 216
      n a i t e k - t k a i v n s p n p f g v m k t e e l s a l g e v c l e h d i l l v s e i y e k l a y g g k k h v
Qy    301 ESTADKNNTATWINPNPCGSVSYDHLSKVAEAKRLGILVIADEVYOKLVLGSAFFI 360
      e s t a d k n n t a t w i n p n p c g s v s y d h l s k v a e a k r l g i l v i a d e v y o k l v l g s a f f i
Db    217 SIAOLSDRLKEQTVIIINGSKSHSMTGWRTGYAAGSE--DIIK-A-N-TNLASH-STSN 269
      s i a o l s d r l k e q t v i i n g s k s h s m t g w r t g y a a g s e - - d i i k - a - n - t n l a s h - s t s n
Qy    361 PMGVFG-HIT-PVLSIGLSKSWIVPWGRWGVAVDPRKILOETKISTITSINYLNVSVD 418
      p m g v f g - h i t - p v l s i g l s k s w i v p w g r w g v a v d p r k i l o e t k i s t i s t i n y l n v s v d
Db    270 PTSAIQYGAIYAANGPSEPL-EEMREAFERHNTIYAKLIEIPGFSCV-KPEGAFYLFPN 327
      p t s a i q y g a i y a a n g p s e p l - e e m r e a f e r h n t i y a k l i e i p g f s c v - k p e g a f y l f p n
Qy    419 PATFIQAALPOILENTKEDFFKAIIGLLKESSEICYKOIKEKNTYITCPRPEGSFMFYMK 478
      p a t f i q a a l p o i l e n t k e d f f k a i i g l l k e s s e i c y k o i k e k n t y i t c p r p e g s f m f y m k
Db    328 AKEAQSCGFQDVDEFVKALLEEKVAIVPGSGSPENVRLSVATSLDLLEEAEIRKR 387
      a k e a q s c g f q d v d e f v k a l l e e k v a i v p g s g s p e n v r l s v a t s l d l l e e a e i r k r
Qy    479 LNLHLE-EIDDDIDFCKLAKESVILCPGSVLGMANWRITFACVPSSLDQDLGRIKS 537
      l n l h l e - e i d d d i d f c k l a k e s v i l c p g s v l g m a n w r i t f a c v p s s l d q d l g r i k s

Db    388 FVERKH 392
      | : : |
Qy    538 FCQRN 542

RESULT          9
ID   PATA_BACSU STANDARD; PRF; 392 AA.
AC   P16524;
DT   01-AUG-1990 (REL. 15, CREATED)
DT   15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
DT   15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE   PUTATIVE AMINOTRANSFERASE A (EC 2.6.1.-).
GN   PATA OR UAT.
OS   BACILLUS SUBTILIS.
OC   BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
OC   BACILLUS.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   SCANLAN-168;
RA   SCANLAN E., DEVINE K.M.;
RL   SUBMITTED (NOV-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
RX   [2]
RP   SEQUENCE OF 361-392 FROM N.A.
RX   MEDLINE: 90094275.
RA   ANTONIEWSKI C., SAVELLI B., STRAGIER P.;
RT   "The spoIIJ gene, which regulates early developmental steps in
RT   Bacillus subtilis, belongs to a class of environmentally responsive
RT   genes.";
RL   J. BACTERIOL. 172:86-93(1990).
CC   -!- COFACTORS: PYRIDOXAL PHOSPHATE (POTENTIAL).
CC   -!- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT
CC   AMINOTRANSFERASES.
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DR	EMBL; AJ322587; E1181905; -	
DR	EMBL; Z95111; E1184990; -	
DR	EMBL; M29450; G143632; -	
DR	SUBTILIST; BG10205; PATA.	
DR	PROSITE; PS00105; AA_TRANSFER_CLASS_1; 1.	
KW	TRANSFERASE; AMINOTRANSFERASE; PYRIDOXAL PHOSPHATE.	
FT	BINDING 230 230	
FT	SEQUENCE 332 AA; 43414 MW; 899A4D38 CRC32;	
SO	SEQUENCE	PYRIDOXAL PHOSPHATE (BY SIMILARITY).

Query Match 8.1%; Score 304; DB 1; Length 392;
Best Local Similarity 23.8%; Pred. No. 5.95e-30;
Matches 97; Conservative 103; Mismatches 180; Indels 28; Gaps 24;

Db	1	MEHLLNPKAREIEISGTR-FESNIVAOHQED--VISLTIGQDPDFTPHHVKAAAKKAIDEN	57
Qy	138	KDGLVLAATGANMSIRAIRYKISASVQEGKRPPLPLAHGDPVSVEPFARTAVEADAFAAA	197
Db	58	V-TS-YTPN-AGY-L-ELRQAVOLYMKKADENYDAESEIIITGQAQIDAAPFTIL-SP	111
Qy	198	VRTQFCNCPYAGVGLPAARSAVAEHUSQGVPMLSADDDVFLTAGGTOAEIVPIVLAQTA	257
Db	112	GDEVIMPPIYGPYEPILINCGAKPVIVD-TTSHGFKLARLEADLTATNTKCVLPYPS	170
Qy	258	GANILLPRGPYPNEYARAFAENRLEVRHFDLIPDKGWEIDIDSLESTADKNTAMVINEN	317
Db	171	NPTGVTLSESELKSIALLLKGRNVFVLSDBIYSELYVDRPHY-SIATYLRDQIV-INGL	228
Qy	318	NPGCSVSYDHLKSKVAEYAKRGLILVIADEVYKGLVGSAPFIPMGVGHITPVLISGLS	377
Db	229	SKSHMTGWRIQFL-FAPKDI--AKHI-LKVHGY-NVSCASSISOKAAL-EAVTNGLDD	281
Qy	378	SKSWIVPGRGLGWAVYDPRKILQETKISTSYTNLVNSTDPAFTFOALPQILENTKED	437
Db	282	AL-IMREQYKRLDYVDRL-VSMGLDVV-KPSGAFYIFPSIK-SF--QWTS-FDFSMAL	334
Qy	438	FFRAIIGLLKESSEICYKIKENKYITCPHKPGSMFVAVKLNHLLEEDIDDDIDFCCKL	497
Db	335	LEDAGVALVPGSSFSFYGEYVRLSFACSMDTUREGLDRLEIFVLKKR	382
Qy	498	AKESVLTCPGSVLGM-AN-WVRITFACYPSSLQDGLGRKIKFSFOCRNK	543

RESULT	10
ID	AATA_RHIME
AC	002635;
STANDARD;	PRT; 400 AA.
DT	01-JUL-1993 (REL. 26, CREATED)
DT	01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
DT	01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
DE	ASPARTATE AMINOTRANSFERASE A (EC 2.6.1.1) (TRANSMINASE A) (ASPAT).
GN	AATA.
DN	RHIZOBIUM MELLIOTT.
OS	BACTERIA; PROTEOBACTERIA; ALPHA SUBDIVISION; RHIZOBIACEAE GROUP;
OC	RHIZOBIACEAE; SINORHIZOBIUM.

RF SEQUENCE FROM N.A.
RX MEDLINE; 91210178.
RA RASTOGI V.K., WATSON R.J.;
RT "Aspartate aminotransferase activity is required for aspartate
RT catabolism and symbiotic nitrogen fixation in *Rhizobium meliloti*.";
RL J. BACTERIOL. 173:2879-2887(1991).

RP SEQUENCE FROM N.A.
RC STRAIN-JJ1C10;
RX MEDLINE; 93209934.
RT WATSON R.J., RASTOGI V.K.;
RT "Cloning and nucleotide sequencing of *Rhizobium* meliloti
RT aminotransferase genes: an aspartate aminotransferase required for
RT symbiotic nitrogen fixation is atypical.";

```

J. BACTERIOL. 175:1919-1928(1993).
-!- FUNCTION: REQUIRED FOR ASYMMETRIC NITROGEN FIXATION.
-!- CATALYTIC ACTIVITY: L-ASPARTATE + 2-OXOGLUTARATE = OXALOACETATE +
  L-GLUTAMATE.
-!- COFACTOR: PYRIDOXAL PHOSPHATE.
-!- SUBUNIT: HOMODIMER (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT
  AMINOTRANSFERASES.
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EMBL; L05064; GI52149; -.
DR PIR; A47094; A47094.
DR PROSITE; PS00105; AA_TRANSFER_CLASS_1; 1.
DR PFAM; PF00155; aminotran_1; 1.
KW TRANSFERASE; AMINOTRANSFERASE; PYRIDOXAL PHOSPHATE.
FT BINDING 239 239 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
SQ SEQUENCE 400 AA; 435582 MW; 7DD47F70 CRC32;

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Query Match	7.7%	Score 287;	DB 1; Length 400;
Best Local Similarity	24.7%;	Pred. No. 4.29e-27;	
Matches	96; Conservative	89; Mismatches 175;	Indels 29; Gaps 23;
Db	26 LKAGG-RDVTGLGAGEDP-FDT-PDNIK-KAADAIDR-CETK-YTPVSGIPELREAIK 79 : : :	: : :	: : :
QY	162 VOEGPPRPVLPLANGDSVPFATVAEADAAAVRTGFNCYPAGVGLPAARSAAVE 221 : : :	: : :	: : :
Db	80 KFKRENLDYYTAAQTIVGTGGKQLIFNAEMATLN--PGDEWVIPAPYWVSYPEKMALCG- 136 : : :	: : :	: : :
QY	222 HLSQGVPYMLSADDVFLTAGGTQAI-EVLIIPVLAQTAGANILLPRCPYNPEARAFNRL 280 : : :	: : :	: : :
Db	137 GTPVFPVPTROENNFKLKAEDLDRAIPTKTFWFNPSPNSPSNGAAYSHHEELKALTVDLMKH 196 : : :	: : :	: : :
QY	281 EVRHFDLI-PDKGEWDIDISLEIAKDNTTAMVIINPNPCGSVSYSDHLKSUKYAE-AKR 338 : : :	: : :	: : :
Db	197 PHVVLTDDMYEHLLTYGDFFATFVEPEGLYERTITMNGVKAYAMTGWRIGYAA--GP 254 : : :	: : :	: : :
QY	339 LGILVIADDEVYGVKLGSAPP-IPMGV-FGHIIPLVLSIGLSRSKWIPGWRLGCWAVIDP 396 : : :	: : :	: : :
Db	255 ---LHLIKAMDMTQO-QOTS-GAASIAQAANAVALNGP-ODFTRKNKEIQGRDLVSM 308 : : :	: : :	: : :
QY	397 RKILOETFKTISTNYNLNVSTDPATEIOARLPOLIENTREDFFEKIAGLLKESSEICYK 456 : : :	: : :	: : :
Db	309 LNOAKGITSCP-TPEGAFYVPSCAGLIGKTAPSCKVIETDEDVESSELTEGVAHVHGSA 367 : : :	: : :	: : :
QY	457 IKENKYITCPHKPEGSFMVMVK-LNL-HLL--EE-IDDDIFCCCLAKEESVILPCGSV 510 : : :	: : :	: : :
Db	368 FGLGNFRISYATSEALLBEACRRIRQC 396 : : :	: : :	: : :
QY	511 LGMANVRITFACVPSLQDGLGRKISFC 539 : : :	: : :	: : :

RESULT	11	ALAT_YEAST	STANDARD;	PRT;	507 AA.
ID	AC	P52892;			
DT	DT	01-OCT-1996	(REL. 34, CREATED)		
DT	DT	01-OCT-1996	(REL. 34, LAST SEQUENCE UPDATE)		
DT	DT	01-NOV-1997	(REL. 35, LAST ANNOTATION UPDATE)		
DE	DE	PUTATIVE ALANINE AMINOTRANSFERASE (EC 2.6.1.2) (GLUTAMIC--PYRUVIC TRANSAMINASE) (GPT) (GLUTAMIC--ALANINE TRANSAMINASE).			
GN	GN	YDR111C OR YD9727.07C.			
OS	OS	SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).			
OC	OC	EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOMYCETES; SACCHAROMYCETALES;			
OC	OC	SACCHAROMYCETACEAE; SACCHAROMYCES.			
RN	RN	[1]			
RP	RP	SEQUENCE FROM N.A.			
RC	RC	STRAIN-S288C / AB972;			

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CC or send an email to license@isb-sib.ch).

DR	EMBL:	Z49335;	G108205;	-
DR	EMBL:	D44603;	G871966;	-
DR	PROSITE:	P500105;	AA-TRANSFER_CLASS_1;	1.
DR	PFAM:	PF00155;	aminotrf_1	1
DR	KW	HYPOTHETICAL PROTEIN; AMINOTRANSFERASE; TRANSFERASE;		
DR	KW	HYPOTHETICAL PHOSPHATE.		
DR	PIBINDING	271 271		
DR	SEQUENCE	444 AA:	50082 MW:	PYRIDOXAL PRC32
DR	SEQUENCE	444 AA:	16ASDF3D	CSC32:

	Query Match	6.7%;	Score 253;	DB 1;	Length 444;
	Best Local Similarity	31.7%;	Pred.	M.1.73e-21;	
	Matches	32;	Conservative	32;	No.matches 34; Indels 3; Gaps 3;
Db	184	WTIDFQFKATISKTAVIINTPHNPKGVFTREELTTLGNTCVKHNVVITSDVEYHL	243		
QY	293	WEIDDSLESIAKDNTAMVINPNPGSVYSYDHLSKVAEYAKRLGILVIADEVYGL	352		
Db	244	YF-TDSFTRIATLSPEIQTLITVGSACKSFAATGWRIGWV	283		
QY	353	VLGSAFFIPMGVFG-HIYFV-LSIGSLSKSWIPGVRLGWV	391		

[illegible]

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DR EMBL; Z69909; E225673; -.
DR PFAM; PF00155; aminotran_1; 1.
KW HYPOTHETICAL PROTEIN; TRANSFERASE; AMINOTRANSFERASE;
KW PYRIDOXAL PHOSPHATE.
FT BINDING 326 326 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
SQ SEQUENCE 505 AA; 56627 MW; 8CD487CF CRC32;

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Query Match      6.7%;   Score 251;   DB 1:   Length 505;
Best Local Similarity 28.7%;   Pred. No. 3.63e-21;
Matches 54;   Conservative 47;   Mismatches 78;   Indels 9;   Gaps 8;

Db 100 PTL-LDHAEEKFQNLPTFDV-VQRSKMLLKESGLSGAYASAGIPLVRHVADFIARD 157
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 169 PVLPLAHHGDSVFPPA-FRTAVEADAAVAARTQFQNCYPAAGVLGAPAAAGVAHELSQGV 227

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QY 323 VYSYDHLKVAEVA-KRLGILVIADVEYKLVLSAPFFIPMGVFGH-IT-PVLSIGSLSK 379
Db 250 AYAMTGWIRIGYAG--GPR-AL--IK-AMAVVOSQATSC-PSSVSOAASVAALNGP-ODEL 301
QY 380 SWIVPGWRLGWAVDPKILQETKISTITNVLNVSTDPATFQAALPQILENTKEDEF 439
Db 302 KERTESFORRNLVNVGLNAIEGLDC-RVPEGAFYTFSGCAGVARRVTPSGKRIESDIDF 360
QY 440 KATIGLKESESEICYKOIRENKYITCPRPEGSMFVNVK-LNL--HEL--EE-IDDDIDF 493
Db 361 CAYLLEDHVAVVPVGSAGLSFYFRISYATSEAEKLEALERISAACKR 408
QY 494 CCKLAKEESVILCPGSLGMANWVRITFACVPSSLODGLGRIKSFQOR 541

Search completed: Fri Oct 1 13:53:55 1999
Job time : 22 secs.


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Db 189 PGIEAMADENTAMVLIINPNPCGVSYDHLKKVAETAATKGLMWITDEVYQOTIPGDK 248
      ::::: || || || || || || || || || || || || || || || || || || || ||
Qy 298 DSLESIAKNTAMVLIINPNPCGVSYDHLKVAEAVAKRLGILVIADEVYKLVLSA 357
      ::::: || || || || || || || || || || || || || || || || || || || ||
Db 249 PFVPMGEFFSITPVITLGGTSKGVWGRIGWLTALNDPRGILKSTGCVOSIQOQLNDITP 308
      ||::|| |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Qy 358 PFIPMGVFGHITPVLSIGSLKSVIWPGRWGVAVYDPRKIQETKISITNVLNVST 417
      ||::|| |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 309 DATIIVQAALPEILGKANKELFAKNSMLKONVELCDRLKEIPCLVCKKKPESCTYLLV 368
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Qy 418 DPATFIAALPOILENTKEDEFFAIGLLKESSEICYKQIKENYITCPHKPEGSMEVMV 477
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 2
ID Q93703 PRELIMINARY; PRT; 464 AA.
AC Q93703;
DT 01-FEB-1997 (TREMBREL. 02, CREATED)
DT 01-FEB-1997 (TREMBREL. 02, LAST SEQUENCE UPDATE)
DT 01-JAN-1999 (TREMBREL. 09, LAST ANNOTATION UPDATE)
DE F42D1.2 PROTEIN.
GN F42D1.2.
OS CAENORHABDITIS ELEGANS.
OC EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
OC RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
RN [1]
RP SEQUENCE FROM N.A.
RA LIGHTNING J.;
RL SUBMITTED (OCT-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 94150718.
RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M., COULSON A.,
RA BONFIELD J., BURTON J., CONNELL M., COPEY T., COOPER J., FULTON L.,
RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., JIER M., JOHNSTON L.,
RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
RA LIGHTNING J., LLOYD C., MCCURRAY A., MORTIMORE B., O'CALLAGHAN M.,
RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULTON J.,
RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans.";
RL NATURE 368:32-38(1994).
DR EMBL; 281081; E1346662; -.
SQ SEQUENCE 464 AA; 51031 MW; A2E3EAB3 CRC32;

Query Match 19.9%; Score 746; DB 5; Length 464;
Best Local Similarity 30.5%; Pred. No. 2.12e-106;
Matches 127; Conservative 126; Mismatches 146; Indels 18; Gaps 17;

Db 45 VLPQSHSKNTVNPVR-KIADACAVPPHPEKKVILKLGDPVSGGKLPPESEIAVOAMHES 103
      ||::|| |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Qy 141 VLAATG-ANMSIRAIKIS-A-SVOEKGRPVLPVLAHGDPSVFPFAFRTAVEAEAVAA 197
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 104 VSSHMEDGYPAGVALAAREAIERYTS-SADNVFTADDVVLASGCSHALQMAIEAVAN-A 161
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Qy 198 VRTGQFNCYPAGVGLPAARSAVAEHLISQGVPMYLSADDVLTAGGTQAEIIVIPVLAQT 257
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 162 GENILVPHGFPPLYSTLCRPHNIVDPYKIDMTGEDVR-IDLSYMATIIDDTKALIVNN 220
      ||::|| |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Qy 258 GANILLPRGYPNYEAR-AAFNRLVRH-FDLIPDKGWEIDSLSESIAKNTAMVIN 315
      ||::|| |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 221 PGNPTGGVTKHELEILAFAHQYKLIITADEIYGLDVLNGATFYPLASLPKVPITCD 280
      ||::|| |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Qy 316 PNPCCSVSYDHLKVAEAVAKRLGILVIADEVYKLVLSAFPFPVFGHITPVLSIG 375
      ||::|| |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 281 GIARKRMVPGWRIGWLIHNFGLVDVKNGI-VALSQKI-VGPCSLVQALPKILRETP 338
      ::::: || || || || || || || || || || || || || || || || || || || ||
Qy 376 SLKSKWIVPGWRIGWLVAVYDPRKIQETKISTITNVLNVSTDPATFIAALPOILENTK 435
      ::::: || || || || || || || || || || || || || || || || || || || ||
Db 339 EDYFVYTRNVIETNANIVSDILADVPMRVV-KPKGAMVMWNIS-R--TAYGSDVSFCQ 394

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Qy 436 EDDFKAILGLLRESSEICYKQIKENYITCPHKPEGSMEVMVKLNHLLEIDDDDFCC 495
      ||::|| |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 395 NLIRESVFP-CLPGQAFSAPGFRVVLTCGSEDMEEAALRIRFEFCYRNFNQHSDES 450
      ::::: || || || || || || || || || || || || || || || || || || || ||
Qy 496 KLAKEESVILC-PGSLVGMANVVRITFACVPSSLODGLGRKISFCORN-KKRNSDD 550
      ::::: || || || || || || || || || || || || || || || || || || || ||

RESULT 3
ID Q33267 PRELIMINARY; PRT; 429 AA.
AC Q33267;
DT 01-JAN-1998 (TREMBREL. 05, CREATED)
DT 01-JAN-1998 (TREMBREL. 05, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBREL. 08, LAST ANNOTATION UPDATE)
DE ASPARTATE AMINOTRANSFERASE.
GN MICY279.04C.
OS MYCOBACTERIUM TUBERCULOSIS.
OC BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIDAE;
OC ACTINOMYCETALES; CORYNEBACTERIACEAE; MYCOBACTERIACEAE; MYCOBACTERIUM.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-H37RV;
RA OLIVER K., HARRIS D.;
RL SUBMITTED (JUL-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-H37RV;
RA PARKHILL J., BARRELL B.G., RAJANDREAM M.A.;
RL SUBMITTED (JUL-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-H37RV;
RX MEDLINE; 96181548.
RA PHILIPP W.J., POULFT S., EIGLMEIER K., PASCOPELLA L.,
RA BALASUBRAMANIAN V., HEYM B., BERGH S., BLOOM B.R., JACOBS W.R. JR.,
RA COLE S.T.;
RT "An integrated map of the genome of the tubercle bacillus,
RT Mycobacterium tuberculosis H37Rv, and comparison with Mycobacterium
RT leprae.";
RL PROC. NATL. ACAD. SCI. U.S.A. 93:3132-3137(1996).
DR EMBL; 297991; E330321; -.
DR PFAM; PF00155; aminotran.1.
KW TRANSFERASE; AMINOTRANSFERASE.
SQ SEQUENCE 429 AA; 47350 MW; 9B68011A CRC32;

Query Match 13.0%; Score 489; DB 2; Length 429;
Best Local Similarity 28.6%; Pred. No. 1.84e-60;
Matches 104; Conservative 93; Mismatches 150; Indels 17; Gaps 17;

Db 41 IRGPVHQHAARLEAEGRH-ILKLNIGNPAPF-GREAPDVIMRDIQALPYAGYSDSGI 98
      ||::|| |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Qy 151 IRAIRYKISASVQEKGRPRVPLAHGDPSPFAPRTAVEAEADAVAAVRTQFNCYPAGV 210
      ||::|| |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 99 -LSARRAVVRYVELVPGFP-RFDVDDVYLGNGVSELIITMTLQALDN-GDQVLIPSPDP 155
      ||::|| |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Qy 211 GLPAARSAVAEH-LSQGVPMYLSADDVLTAGGTQAEIIVIPVLAQTAGANILLPRGYP 269
      ||::|| |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 156 LWTASTSAGGTPVHY-ICDETQGHQPIADLESKITER-TKALVVINPNPTGAVYSCE 213
      ||::|| |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Qy 270 NYEARAAFNRLVRHFDLIPDK-GWEIDIDSLSES-IADKNTAMVLIINPNPCGVSYD 327
      ||::|| |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 214 ILTQVMDIARHQLLLADLADLADLADLADLADLADLADLADLADLADLADLADLADL 273
      ||::|| |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Qy 328 HUSKVAEAVAKRLGILVIADEVYKLVLSAFPFPVFGHITPVLSIGSLKSWIVPGWR 387
      ||::|| |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 274 AGWLAITGPKHEHASSFIEGIGILLANRLCPNVPAQHAIOVALGG-HQST-EDLVLPGRRL 331
      ||::|| |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Qy 388 LGWVAVDPRKILQETKISTITNVLNVSTDPATF-IOAALPQILENTKEDEFFAIIGL 445
      ||::|| |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 332 L-EQRDIATWTKLNEIPGVSCV-KPAGALYAFRLDPEVVD-IDDDLEQLVLDLLSEKILV 388
      ||::|| |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Qy 446 LKESSEICYKQIKENYITCPHKPEGSMEVMVKLNHLLEIDDDDFCCCKLAKEESVIL 505

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Db 389 TOGT 392
QY 506 CPGS 509

RESULT 4
ID 086587; PRELIMINARY; PRT; 402 AA.
AC 086587;
DT 01-NOV-1998 (TREMBREL. 08, CREATED)
DT 01-NOV-1998 (TREMBREL. 08, LAST SEQUENCE UPDATE)
DE PUTATIVE AMINOTRANSFERASE.
GN SC2H4.04C.
OS STREPTOMYCES COELICOLOR.
OC BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIDAE;
OC ACTINOMYCETALES; STREPTOMYCINAE; STREPTOMYCETACEAE; STREPTOMYCES.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-A3(2);
RA OLIVER K., HARRIS D.;
RL SUBMITTED (SEP-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-A3(2);
RA PARKHILL J., BARRELL B.G., RAJANDREAM M.A.;
RL SUBMITTED (SEP-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-A3(2);
RX MEDLINE: 97000351.
RA KINASHI H., HOPWOOD D.A.;
RA REDENBACH M., KIESER H.M., DENAPALTE D., EICHNER A., CULLUM J.,
RT the 8 Mb Streptomyces coelicolor A3(2) chromosome.
RL MOL. MICROBIOL. 21:77-96(1996).
DR EMBL; AL031514; E1319222.
KW TRANSFERASE; AMINOTRANSFERASE.
SQ SEQUENCE 402 AA; 44448 MW; 185FB18E CRC32;

Query Match 12.4%; Score 466; DB 2; Length 402;
Best Local Similarity 27.2%; Pred. No. 1.91e-56;
Matches 105; Conservative 107; Mismatches 155; Indels 19; Gaps 17;

Db 24 ANALEEAG-HSVLRNTGNPALF-GFEAPEIVQDMIRMLPRAH-G-YTDSRGILSARRA 79
QY 159 SASVOEKGRPVLPVLAHGDPSPVFAFTAVEADAATAAATGQFCYAGVGLPAARSA 218
Db 80 VAQRY-QALGLEVDVDDVFLGNGYSELISMAVQALLE-DCDEVLLPAPDFPLTAVTTLA 137
QY 219 VAHLSQGVPMLSADDDVFLTAGTQALEVLPVLAQTAGANILLPRGYPNVEARAFN 278
Db 138 GKAVHY-LCDEQAEWYPDLADMEAKITDR-TKAVIINPNPTGAVYKPEIVEGILDLA 195
QY 279 RLEVRHFDLPDKG-WEIDIDSL- IADKNTTAMVINPNPCGSVSYDHLKVAEVA 336
Db 196 RHGLMWLADIIQILYDDAVHISAASLAPDLVLTFCGLSKTYRVAGFRSGWLVTGP 255
QY 337 KRLGILVIADIEVYKLVLSGAPFPVPMGVFGHITPVLSIGLSKSWIVPGWRLGWAVYDP 396
Db 256 KOHARDYLEGTLMLASRLCANAPQAQIAOALGGR-QSIRE--LTAPGGRLEHQRDVAW 312
QY 397 RKILQETKISTSIYNLVSTP-PATF-IQALPQILENTKEDFFKAIIGLLKESSEICY 454
Db 313 EKLNEIPGISCV-KPGKALYAFPRID-PAVHKIHDDERFVLDLILREKIQVQGTGFNWP 370
QY 455 KQIKENYITCPHKEGSMFVWVWKLNLHLEIDDDIDFCCCKLAKESVILCPGVLG-- 512
Db 371 SPDHFRLTLPHADLEAAIGRICRF 396
QY 513 MANWVRITFACVPSLQDGLGRKSF 538

RESULT 5
ID 059044; PRELIMINARY; PRT; 401 AA.
AC 059044;
DT 01-AUG-1998 (TREMBREL. 07, CREATED)
DT 01-AUG-1998 (TREMBREL. 07, LAST SEQUENCE UPDATE)
DT 01-JAN-1999 (TREMBREL. 09, LAST ANNOTATION UPDATE)
DE 401AA LONG HYPOTHETICAL ASPARTATE AMINOTRANSFERASE.
GN PH1322.
OS PYROCOCUS HORIKOSHII.
OC ARCHAEA; EURYARCHAEOTA; THERMOCOCCALES; THERMOCOCCACEAE; PYROCOCUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-OT3;
RX MEDLINE: 98344137.
RA KAWARABAYASI Y., SAWADA M., HORIKAWA H., HAIKAWA Y., HINO Y.,
RA YAMAMOTO S., SEKINE M., BABA S., KOSUGI H., HOSOIYAMA A., NAGAI Y.,
RA SAKAI M., OGURA K., OTURA R., NAKAZAWA H., TAKAMIYA M., OHFUKU Y.,
RA FUNAHASHI T., TANAKA T., KUDOH Y., YAMAZAKI J., KUSHIDA N., OGUCHI A.,
RA AOKI K., NAKAMURA Y., ROBB T.F., HORIKOSHI K., MASUCHI Y., SHIZUYA H.,
RA KIKUCHI H.;
RT "Complete Sequence and Gene Organization of the Genome of a
RT Hyper-thermophilic Archaeobacterium, Pyrococcus horikoshii Ot3.";
RL DNA RES. 5:55-76(1998).
DR EMBL; AP000006; D1031371.
KW TRANSFERASE; AMINOTRANSFERASE.
SQ SEQUENCE 401 AA; 45564 MW; 01CD3533 CRC32;

Query Match 12.2%; Score 457; DB 1; Length 401;
Best Local Similarity 29.0%; Pred. No. 7.01e-55;
Matches 93; Conservative 83; Mismatches 132; Indels 13; Gaps 12;

Db 28 LEKKGIK-VIRLNIQDPVAF-DFQPPHMKAEYCAIOEGH-NYYGDSEGLLEAEIVK 84
QY 162 VQEKGRPVLPVLAHGDPSPVFAFTAVEADAATAAATGQFCYAGVGLPAARSAVAE 221
Db 85 RKEKNGVDITDDVVRVTAATEALQIFGALLD-PGDEILIPGSPYPTGLVRFYGGK 143
QY 222 HLSQGVPMLSADDDVFLTAGTQALEVLPVLAQTAGANILLPRGYPNVEARAFNRL 281
Db 144 PVEYRTIEEGWQPDIDDLRKKISER-TKAIIVINPNPTGALYDKKITEEIIINVAEHD 202
QY 282 VRHFDLPDKGWEIDIDSL-ESIADKNTTAMVINPNPCGSVSYDHLKVAEYAKRLG 340
Db 203 LVVLSDIEIYDLMTYEGKHISP-GSLTKDVPVIMVNGLSKVYFATGRLGYMVFVDEPKL 261
QY 341 ILVIADEVYKLVLSGAPFPVPMGVFGHITPVLSIGLSKSWIVPGWRLGWAVYDPKRL 400
Db 262 SEVRRAIDKLARICPNTPQOF--AAIAG-LTGSW-DYLKEYMKKLKRRDFYKRLNE 317
QY 401 QETKISTSIYNLVSTP-PATFIIQALPQILENTKEDFFKAIIGLLKESSEICYKQIKE 459
Db 318 IPGIS-TTKPGCAFYIFPRIE 337
QY 460 NKYITCPHKEGSMFVWVWKLN 480

RESULT 6
ID P71348; PRELIMINARY; PRT; 404 AA.
AC P71348;
DT 01-FEB-1997 (TREMBREL. 02, CREATED)
DT 01-FEB-1997 (TREMBREL. 02, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBREL. 08, LAST ANNOTATION UPDATE)
DE ASPARTATE AMINOTRANSFERASE (ASPC).
GN HI0286.
OS HAEMOPHILUS INFLUENZAE.
OC BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; PASTEURELLACEAE;
OC HAEMOPHILUS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 95350630.
RA FLETSCHMANN R.D., ADAMS M.D., WHITE O., CLAYTON R.A., KIRKNESS E.F.,
RA KERLAVAGE A.R., BULT C.J., TOMB J.F., DOUGHERTY B.A., MERRICK J.M.,
RA MCKENNEY A., SUTTON G., FITZHUGH W., FIELDS C.A., GOCAYNE J.D.,
RA SCOTT J.D., SHIRLEY R., LIU L.I., GLODEK A., KELLEY J.M.,
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RA WEIDMAN J.F., PHILLIPS C.A., SPRIGGS T., HEDBLOM E., COTTON M.D.,
 RA UTTERBACK T.R., HANNA M.C., NGUYEN D.T., SAUDEK D.M., BRANDON R.C.,
 RA FINE L.D., FRITCHMAN J.D., FUHRMANN J.L., GEOGHAGEN N.S.M.,
 RA GNEHM C.L., McDONALD L.A., SMALL K.V., FRASER C.M., SMITH H.O.,
 RA VENTER J.C.;
 RT "Whole-genome random sequencing and assembly of Haemophilus
 RT influenzae Rd";
 RL SCIENCE 269:496-512(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA L TATISOV R., MUSEGHEGAN A.R., BORK P., BROWN N.P., HAYES W.S.,
 RA BORDOVSKY M., RUDD K.E., KOONIN E.V.;
 RL CURR. BIOL. 6:279-291(1996).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA FLEISCHMANN R.D., ADAMS M.D., WHITE O., CLAYTON R.A., KIRKNESS E.F.,
 RA KERLAVAGE A.R., BULT C.J., TOMB J.F., DOUGHERTY B.A., MERRICK J.M.,
 RA MCKENNEY K., SHUTTON G., FITZHUGH W., FIELDS C.A., GOCAYNE J.D.,
 RA SCOTT J.D., SHIRLEY R., LIU L.I., GLODEK A., KELLEY J.M.,
 RA WEIDMAN J.F., PHILLIPS C.A., SPRIGGS T., HEDBLOM E., COTTON M.D.,
 RA UTTERBACK T.R., HANNA M.C., NGUYEN D.T., SAUDEK D.M., BRANDON R.C.,
 RA FINE L.D., FRITCHMAN J.L., FUHRMANN J.L., GEOGHAGEN N.S.M.,
 RA GNEHM C.L., McDONALD L.A., SMALL K.V., FRASER C.M., SMITH H.O.,
 RA VENTER J.C.;
 RL SUBMITTED (JUL-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA WHITE O., CLAYTON R.A., KERLAVAGE A.R., FLEISCHMANN R.D.;
 RL SUBMITTED (SEP-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: U32714; G1573250; -
 DR PFAM: PF00155; aminotran_1; 1.
 KW TRANSFERASE; AMINOTRANSFERASE.
 SQ SEQUENCE 404 AA; 45160 MW; 8082209D CRC32;
 Query Match 11.5%; Score 433; DB 2; Length 404;
 Best Local Similarity 26.1%; Pred. No. 1.00e-50;
 Matches 103; Conservative 106; Mismatches 166; Indels 20; Gaps 19;
 Db 17 IRGPHVKEALRLKEEGNK-TLKNIGNPAPF-GFEAPDEILVDVLRNLSAQ-G-YCDSK 72
 QY 151 IRAIRKISASVQEKGRPVLPVLAHGDPSVFPAPRTAVEADAVAARTGQNCYPAGV 210
 Db 73 GLXSARKAIQYQSKGI-LGATVNDVYIGNGVSELITMAMQALLN-DGDEVLPMPDYP 130
 QY 211 GLPAARSVAEHL-SQGVPMLSADDVLTAGTQAEIVIPVLAQTAGANILLPRGPY 269
 Db 131 LWTAAVTLGSKGAVHY-LCDEDANWFTIDDIKAKVNAKTKAIVINPNPTGAVYSKEL 189
 QY 270 NYEARAAFNRLVRFHFDLPDKG-WEIDIDSLESIAADKNTAMVINPNPCGSVYSYDH 328
 Db 190 LQEIETARONNLIITADEYDKILVDGAVHHIAALAPDLLTTLNGLSKAYRVAGFRQ 249
 QY 329 LSKVAEAKRLGLVIADEVYGLVLSAFPIPMGVFGHTIPVLSIGLSKSWIVPGWRL 388
 Db 250 GWMILNGPKHNAKYIEGLDMLASMRICANVPMQHAITQALGY-OSINE-FILPGRL 307
 QY 389 GWAVYDPRKILQETKISTITNYLVNSTD-PATF-IQAALPQILENTKEDFFKAIIGLL 446
 Db 308 EQRNKA-YDILTIQIPGTCV-KPMGAMYPEKIDVKFN-IHSDKRVLLDLROEKVLLV 364
 QY 447 KESSEICYKQIKENKYITCPHKPEGSFMVVKLNHLLEEDIDDDIDFCCKLAKEESVILC 506
 Db 365 HGKGFNNHSDPHFRIVLPYV-NOLEBAITKLARF 398
 QY 507 PGSVILG--MANWVRI-TFACVPSSLDQGLGRIKSF 538
 RESULT 7
 ID O88124 PRELIMINARY; PRT; 402 AA.
 AC O88124;
 DT 01-NOV-1998 (TREMBLREL. 08, CREATED)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)

DE PUTATIVE AMINOTRANSFERASE.
 GN STGA.
 OS STREPTOMYCES ANULATUS.
 OC BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIDAE;
 OC ACTINOMYCETALES; STREPTOMYCINAE; STREPTOMYCETACEAE; STREPTOMYCES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA TERCERO J.A., ESPINOSA J.C., JIMENEZ A.;
 RT "Strg, a new Streptomyces alboniger member of the LysR family of
 RT transcriptional regulators";
 RL SUBMITTED (JUN-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: AJ006517; E1318411; -
 DR EMBL: AJ005198; E1318407; -
 KW TRANSFERASE; AMINOTRANSFERASE.
 SQ SEQUENCE 402 AA; 44414 MW; 5CD3256A CRC32;
 Query Match 11.1%; Score 415; DB 2; Length 402;
 Best Local Similarity 27.2%; Pred. No. 1.26e-47;
 Matches 105; Conservative 99; Mismatches 161; Indels 21; Gaps 16;
 Db 24 ANALEEAG-HSVLRNLNTGNPALF-GF-EA--PEEIVQDMIRMLPQAHGYTDSRGVLSARR 78
 QY 159 SASVQEKGRPVLPVLAHGDPSVFPAPRTAVEADAVAART-GQFNCYPAGVGLPAARS 217
 Db 79 AVAQRYQALGLD-EVSVDDVFLNGVSELVTMAVOALLE-DGDEILIPAPDFPLTAVTT 136
 QY 218 AVAEHL-SQGVPMLSADDVLTAGTQAEIVIPVLAQTAGANILLPRGPYPNTEARAA 276
 Db 137 LSGGRAVHYVDEADADWYFDLDDMSKITDOTKAVEIINPT--GAVYPKEILEGILDA 193
 QY 277 FNRLEVRHFDLPDKGWEIDIDSLESIAADKNTAMVINPNPCGSVYSYDHLKVAEVA 336
 Db 194 RRHGLMFADEIYDQILYDDAVHSHVAALAPDLVLTFCGLSKTYRVAGFRGWLVTGP 253
 QY 337 KRLGLIIVIADEVYGLVLSAFPIPMGVFGHTIPVLSIGLSKSWIVPGWLGWAVYDP 396
 Db 254 ROHARDYLEGLTMLASMRICPNAPQAFQALQALGR-OSIRE--LTAPGGAHGEQDRAW 310
 QY 397 RKILQETKISTITNYLVNSTD-PATF-IQAALPQILENTKEDFFKAIIGLKESEICY 454
 Db 311 EKLINEIPGVSCV-KPKGALYAFPRIDPKY-HPIHDDKRFVLDLLQEKIQVYVQGTGFNWP 368
 QY 455 KOIKENKYITCPHKPEGSFMVVKLNHLLEEDIDDDIDFCCKLAKEESVILCPGVLG-- 512
 Db 369 RPDHFRILTPHADDDRAISGRIF 394
 QY 513 MANWVRIEACVPSSLDQGLGRIKSF 538
 RESULT 8
 ID O67781 PRELIMINARY; PRT; 394 AA.
 AC O67781;
 DT 01-AUG-1998 (TREMBLREL. 07, CREATED)
 DT 01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE ASPARTATE AMINOTRANSFERASE.
 GN ASPL1.
 OS AQUIFEX AEOLICUS.
 OC BACTERIA; AQUIFICALES; AQUIFICACEAE; AQUIFEX.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=VF5;
 RX MEDLINE; 98196666.
 RA DECKERT G., WARREN P.V., GAASTERLAND T., YOUNG W.G., LENOX A.L.,
 RA GRAHAM D.E., OVERBEEK R., SNEAD M.A., KELLER M., AUJAY M., HUBER R.,
 RA FELDMAN R.A., SHORT J.M., OLSON G.J., WANSON R.V.;
 RT "The complete genome of the hyperthermophilic bacterium Aquifex
 RT aeolicus";
 RL NATURE 392:353-358(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=VF5;
 RA DECKERT G., WARREN P.V., GAASTERLAND T., YOUNG W.G., LENOX A.L.,

RA GRAHAM D.E., OVERBEEK R., SNEAD M.A., KELLER M., AUJAY M., HUBER R.,
RA FELDMAN R.A., SHORT J.M., OLSON G.J., SWANSON R.V.,
RL SUBMITTED (JUL-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR ENBL: AE000766; G2984217;
KW TRANSFERASE; AMINOTRANSFERASE.
SQ SEQUENCE 394 AA; 43777 MW; B9D83011 CRC32;

Query Match 10.7%; Score 402; DB 2; Length 394;
Best Local Similarity 28.2%; Pred. No. 2.13e-45;
Matches 103; Conservative 95; Mismatches 139; Indels 28; Gaps 26;

Db 42 PFDTPDFKEACIRALRGKTK-YAPSAGIPELREATAEKLLKENKVEYK-PSEIV-VS 98
QY 182 PAFRTAVEAEDAVAAAVRTGQFNCYPAGVGLPAARSVAEHL-SQG-VPYMLSDDDVFLT 239
Db 99 AGAKMVLIFMAILDE--GDEVLLPSYWVTPQIRFFGGVPV-EVPLKKEKGFQSL 155
QY 240 AGGTQAI-EVILPVAQTAGANILLPRCPYNYEARAF-NRLEYRHFDLIPDKGWEIDI 297
Db 156 EDVKEKTER-TRAVINSPNPTGAVYEEELKIAECVER-GIFISDECIEFYVG 213
QY 298 DSL-ESIAKNTTAMVIINPNPCGVSVDYHLSKVAEV-AKRLGILVIADEVYGLVIG 355
Db 214 DAKFVSPASDEVKNTITFVAFSKSYMTGWRIGYVA-C-P-E-EVAKVIALSN-Q 267
QY 356 SAFIPMGVGH-ITPV-LSIGLSKSWIVPGWGLGWAVYDPKILQETKISTITNYL 413
Db 268 SVS-NVTTFAQAL-EALKNPKSKDFVNMENAFERRRDTAVELSKIPGMVYV-KPEG 324
QY 414 NVSTDPAFTIQ-AALPQILENTKE-DFFKAIIGLLKESSEICYKQIKENKYITCPHKPEG 471
Db 325 AFVIFPDPSAVA-EKLGDDVKLSEFLERAKVAVVPGSAGFAPGLRLSYALSEERLVEG 383
QY 472 SMFVWVKNLHLEEDDDIDFCKLAKEESVILCPGSLGMVNVRTTFCVPSLQDG 531
Db 384 IRIK 388
QY 532 LGRIK 536

RESULT 9 PRELIMINARY; PRT; 405 AA.
ID P77727;
AC P77727;
DT 01-FEB-1997 (TREMBREL. 02, CREATED)
DT 01-FEB-1997 (TREMBREL. 02, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBREL. 08, LAST ANNOTATION UPDATE)
DE FROM BASES 2401667 TO 2412529
DE (SECTION 208 OF 400) OF THE COMPLETE GENOME (SECTION 208 OF 400).
OS ESCHERICHIA COLI.
OC BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; ENTEROBACTERIACEAE;
OC ESCHERICHIA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-K-12;
RA BLATTNER F.R., PLUNKETT G. III, MAYHEW G.F., PERNA N.T.,
RA GLASNER F.D.;
RL SUBMITTED (JAN-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-K12;
RA AIBA H., BABA T., FUJITA K., HAYASHI K., HONJO A., HORIUCHI T.,
RA IKEMOTO K., INADA T., ISONO K., ISONO S., ITOH T., KANAI K., KASAI H.,
RA KASHIMOTO K., KIM S., KIMURA S., KITAGAWA M., KITAKAWA M., MAKINO K.,
RA MASUDA S., MIKI T., MIZOBUCHI K., MORI H., MOTOMURA K., NAKAMURA Y.,
RA NASHIMOTO H., NISHIO Y., OSHIMA T., SAITO N., SAMPEI G., SEKI Y.,
RA TAGAMI H., TAKEMOTO K., WADA C., YAMAMOTO Y., YANO M.,
RL SUBMITTED (JAN-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR ENBL: AE000318; G1788627;
DR EMBL: D90860; G1799660;
DR PFAM: PF00155; aminotran.1;
KW TRANSFERASE; AMINOTRANSFERASE.
SQ SEQUENCE 405 AA; 45517 MW; DF062CD9 CRC32;

Query Match 10.6%; Score 399; DB 2; Length 405;
Best Local Similarity 26.3%; Pred. No. 6.94e-45;
Matches 96; Conservative 99; Mismatches 154; Indels 16; Gaps 16;

Db 17 IRGPVLKEAKRLEEBGNK-VLKLNIGNPAPF-GFDAPDELIVDIRLPTAQ-G-YCDK 72
QY 151 IIRAIYKISASVOEKGRPRVPLAHGDSVPFPAFTAVEAEDAVAAAVRTGQFNCYPAGV 210
Db 73 GLYSARKALIMQHYQARGMRDV-TVEDIYVINGVSELIVQAMQALLNS-GDEMLVPADYP 130
QY 211 GLPAARSVAEHL-SQGVPMLSADDVLTAGGTQAEVIVPVAQTAGANILLPRGYP 269
Db 131 LMTAVSLSKGVAVY-LCDESSWFFDLDIRAKITPRTRGIVIIINPNPTGAVISKEL 189
QY 270 NYEARAARNRLEHFDLIPDKG-WEIDISLEADKNTTAMVIINPNPCGVSVDYH 328
Db 190 LMEIVEIAROHNLIIFADEIYDKILYDDAEHSIAPLAPDLLITTFNGLSKTYRVAGFRQ 249
QY 329 LSKVAEAKRGLIIVIADEVYGLVGSAPFIPMGVFGHITPVLSIGLSKSWIVPGWRL 388
Db 250 GWMVLNPKKHAQVIEGLEMLASRLCANVPAQHAQTALGGY-QSISE-FITPG-GR 306
QY 389 GWAVYDPRKILQETKISTITNLVSTD-PATF-IOAALPQILENTKEDFFKAIIGLL 446
Db 307 YQORNRWELINDIPGVCV-KPRGALYMEPKIDAKREN-IHDDQKMWLDPLQEKVLL 364
QY 447 KESSEICYKQIKENKYITCPHKPEGSMFVWVKNLHLEEDDDIDFCKLAKEESVILC 506
Db 365 QGTAF 369
QY 507 PGSVL 511

RESULT 10 PRELIMINARY; PRT; 397 AA.
ID O53870;
AC O53870;
DT 01-JUN-1998 (TREMBREL. 06, CREATED)
DT 01-JUN-1998 (TREMBREL. 06, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBREL. 08, LAST ANNOTATION UPDATE)
DE PUTATIVE AMINOTRANSFERASE.
GN MT043 51C
OS MYCOBACTERIUM TUBERCULOSIS.
OC BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIACEAE;
OC ACTINOMYCETALES; CORYNEBACTERIACEAE; MYCOBACTERIACEAE; MYCOBACTERIUM.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-H37RV;
RA HAMLIN N., CHURCHER C.M.;
RL SUBMITTED (FEB-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-H37RV;
RA COLE S.T., PARKHILL J., BARRELL B.G., RAJANDREAM M.A.;
RL SUBMITTED (FEB-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-H37RV;
RX MEDLINE; 96181548.
RA PHILIPP W.J., POULET S., EIGLMEIER K., PASCOPELLA L.,
RA BALASUBRAMANIAN V., HEYM B., BERGH S., BLOOM B.R., JACOBS W.R. JR.,
RA COLE S.T.;
RT "An integrated map of the genome of the tubercle bacillus,
RT Mycobacterium tuberculosis H37Rv, and comparison with Mycobacterium
RT leprae";
RL PROC. NAIL. ACAD. SCI. U.S.A. 93:3132-3137(1996).
DR EMBL: AL022004; E1254000;
KW TRANSFERASE; AMINOTRANSFERASE.
SQ SEQUENCE 397 AA; 42209 MW; 447498CB CRC32;

Query Match 9.6%; Score 359; DB 2; Length 397;
Best Local Similarity 32.5%; Pred. No. 4.21e-38;
Matches 66; Conservative 51; Mismatches 79; Indels 7; Gaps 7;

[illegible]

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QY 168 RPVLPLAHGDPSPVPAFTAVEADAADVAAVRTGQNCYPCAGVGLPAARSVAEHLSCQV 227
Db 84 GYEVAESQVLVTNGGKQAIYFAAAIL-D-PGDEVIVPAPYWTYTYPESIRLAG-GVP-VD 139
QY 228 PYMLSADDDVFLTAGTQAI-EVIIPVLAQVAGANILLPRPGYNYEARAAFNRLVRHFD 286
Db 140 VVADETGTYRVSVEQLAARTERKVVLFVSPNSPTGVSYSSEADAKAIGEWAAEHGLWL 199
QY 287 LIPD-KGWEIDIDSLIESIADKNTAMVIINPNPCGVSYSYDHLKVAEVAKRGLIYI 344
Db 200 TDEYEHLYVGEAKFTSLPLVLPALDKCIIVNGVAKTYAMTGWVGV-I-APQDVIA 257
QY 345 ADEYIGKLVLSAPFIPMGVFGH-ITP-VLSIGLSKSWIVPGWGLGWAVYDPRKILQE 402
Db 258 ATNLQSHATS-NVGNVAQVAALAAVSNLDV-AEMKAF-DRRROT-M-V--KMLNEIDG 311
QY 403 TKISTSIYNLVSTDPATFIOALPOILENTKEDFKAIIGLLKSESSEICYKIKENKY 462
Db 312 VFPC-TPEGAFYAVPSKELLGKIRKQSSVELAAILDEVEVAVVPGFAFGPGYL 370
QY 463 ITCPKKPEGSFV-MVK--LNLHLEEI-DDDIDFCCKLAKEESVILCPGSLGNAVNV 517
Db 371 RLSVALGDEDLVEGVSRI 388
QY 518 RITFACVPSSLODGLGRI 535

RESULT 13
ID O25383 PRELIMINARY; PRT; 390 AA.
AC O25383;
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE SOLUTE-BINDING SIGNATURE AND MITOCHONDRIAL SIGNATURE PROTEIN (ASPB).
GN HP0672.
OS HELICOBACTER PYLORI (CAMPYLOBACTER PYLORI).
OC BACTERIA; PROTEOBACTERIA; EPSILON SUBDIVISION; HELICOBACTER GROUP;
OC HELICOBACTER.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-A3(2);
EX MEDLINE; 97394467.
RA TOMB J.-F., WHITE O., KERLAVAGE A.R., CLAYTON R.A., SUTTON G.G.,
RA FLEISCHMANN R.D., KETCHUM K.A., KLENK H.-P., GILL S., DOUGHERTY B.A.,
RA NELSON K., QUACKENBUSH J., ZHOU L., KIRKNESS E.F., PETERSON S.,
RA LOFTUS B., RICHARDSON D., DODSON R., KHALAK H.G., GLODEK A.,
RA MCKENNEY K., FITZGERALD L.M., LEE N., ADAMS M.D., HICKEY E.K.,
RA BERG D.E., GOCAYNE J.D., UTTERBACK T.R., PETERSON J.D., KELLEY J.M.,
RA COTTON M.D., WEIDMAN J.M., FUJII C., BOWMAN C., WATTHEY L., WALLIN E.,
RA HAYES W.S., BORODOVSKY M., KARP P.D., SMITH H.O., FRASER C.M.,
RA VENTER J.C.;
RT "The complete genome sequence of the gastric pathogen Helicobacter
pylori (published erratum appears in Nature 1997 Sep
RT 25:389(6649):412).";
RL NATURE 388:539-547(1997).
DR EMBL; AE000580; G2313794; -.
DR TIGR; HP0672; -.
DR PFAM; PF00155; aminotran_1; 1.
KW HYPOTHETICAL PROTEIN.
SQ SEQUENCE 390 AA; 42874 MW; BAD53859 CRC32;

Query Match 9.4%; Score 353; DB 2; Length 390;
Best Local Similarity 25.8%; Pred. No. 4.29e-37;
Matches 93; Conservative 86; Mismatches 163; Indels 19; Gaps 17;

Db 40 PDFDTPQAIKDAIKALNDG-FTKYPVAGIPPELLKAIKAKKKNLNDYEPNELVNSG 98
QY 182 PAFRTAVEADAADVAAVRTGQNCYPCAGVGLPAARSVAEHLSCQVYMLSDDDVFLTAG 241
Db 99 AKQSLFNAIQALIE-EGDEVIVPFWTYTPYELVKYS-GYSQFIQTDEKSHFKITPKQL 156
QY 242 GTQAEIIVPVAQVAGANILLPRPGYNYEARAAFNRLVRHFDLIPDKG-WEIDIDSL 300
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Db 157 KDALSPK-TKMLILTTSPNFTGMLYSKAELEVLGEVLKDTKWVWLSDEIYEKLYV-KGEF 214
QY 301 -ESADAKNTAMVIINPNPCGVSYSYDHLKVAEVAKRGLIYIADDEVYKLVLSGSAFF 359
Db 215 VSCAAVESEEMKKRTITISGLSKSVAMTGWRMGYAASKDKLVKLMNLSOQTSNINSIT 274
QY 360 IP-MGVEGHIT-PVLSIGLSKSWIVPGWGLGWAVYDPRKILQETKISTSIYNLVST 417
Db 275 QMAS-I-VAL-EGLYD-KE--IETMQAFERRCDLAHAKINAIGGLN-ALKPDGAEYLEI 327
QY 418 DPATFIOAALPOILENTKEDFFKAIIGLLKSESSEICYKIKENKYITCPHKKPEGSFV 477
Db 328 HIG-SLGC--GDSMRFFCHELLEKEGVALVPGKAFGLGEGYVRLSFACSESEQIEKIERIAR 384
QY 478 KLNHLLEEDDDIDFCCKLAKEESVILCPGSLGNAVNVRTITFACVPSLQDGLGRIKS 537
Db 385 F 385
QY 538 F 538

RESULT 14
ID O54170 PRELIMINARY; PRT; 382 AA.
AC O54170;
DT 01-JUN-1998 (TREMBLREL. 06, CREATED)
DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE AMINOTRANSFERASE.
GN SC7H1.11.
OS STREPTOMYCES COELICOLOR.
OC BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIDAE;
OC ACTINOMYCETALES; STREPTOMYCINAE; STREPTOMYCETACEAE; STREPTOMYCES.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-A3(2);
RA MURPHY L., HARRIS D.;
RL SUBMITTED (JAN-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-A3(2);
RA PARKHILL J., BARRELL B.G., RAJANDREAM M.A.;
RL SUBMITTED (JAN-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-A3(2);
RX MEDLINE; 97000351.
RA REDENBACH M., KIESER H.M., DENAPAITTE D., EICHNER A., CULLUM J.,
RA KINASHI H., HOPWOOD D.A.;
RT "A set of ordered cosmids and a detailed genetic and physical map for
the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
RL MOL. MICROBIOL. 21:77-96(1998).
DR EMBL; AL021411; E1245740; -.
KW TRANSFERASE; AMINOTRANSFERASE.
SQ SEQUENCE 382 AA; 40860 MW; 9FCBF75A CRC32;

Query Match 9.0%; Score 337; DB 2; Length 382;
Best Local Similarity 25.7%; Pred. No. 2.03e-34;
Matches 79; Conservative 81; Mismatches 134; Indels 13; Gaps 10;

Db 1 MIATPPASRIAEELRRSRPALAPPAGVSLANGEPD-FPTPTVVQA--AVSA-LREG 56
QY 142 LAATGANNMSIRAIRYKISASVQEKGRPVLPLAHGDPSPVPAFTAVEADAADVAAVRTG 201
Db 57 HTH-YADQGRLELRALAAALPERPGAMDDDLVTHGATAALAAV-LATVGPQDRV 114
QY 202 QFNCPAGVGLPAARSVAEHLSCQVYMLSDDDVFLTAGTQAEIIVPVAQTAGANI 261
Db 115 VYPEPAYSLYADLVVLAGTVDFTVPLADLHW--DLALAAALP-GAAMMIFSNPSNPTG 171
QY 262 LLRPGYNYEARAAFNRLVRHFDLIPDKGWEIDIDSLIESIADKNTAMVIINPNPCG 321
Db 172 IVHREELEALGKLIDGTDVLVWSDEAYHRLAYPGHPVSALEIESLRGRVTVQTESKT 231
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QY 322 SVSYDHLKVAEAKRILGILVIADENVYKLVL-GSAPFIPMGVFGHTIPVLSIGSLKS 380
Db 232 YAMTGRVGYLT--CPREVLDAAQVHTWNGSLNTAVOHAALALDLPDGVGVAMADRY 289
QY 381 WTVPGRWLGWAVYDPKILQET-KISTSYTNLYNVSTDPATFIOALFOILENTKEDFF 439
Db 290 RQRDLV 296
QY 440 KAIIGLL 446

RESULT 15
ID O28151 PRELIMINARY; PRT; 379 AA.
AC O28151;
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE ASPARTATE AMINOTRANSFERASE (ASPB-2).
GN AF2129.
OS ARCHAEOGLOBUS FULGIDUS.
OC ARCHAEA; EURYARCHAEOTA; ARCHAEOGLOBALES; ARCHAEOGLOBACEAE;
OC ARCHAEOGLOBUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-VC-16 / DSM 4304 / ATCC 49558;
RX MEDLINE; 98049343;
RA KLENK H.-P., CLAYTON R.A., TOMB J.-F., WHITE O., NELSON K.E.,
RA KETCHUM K.A., DODSON R.J., GWINN M., HICKEY E.K., PETERSON J.D.,
RA RICHARDSON D.L., KERLAGE A.R., GRAHAM D.E., KYRIDES N.C.,
RA FLEISCHMANN R.D., QUACKENBUSH J., LEE N.H., SUTTON G.G., GILL S.,
RA KIRKNESS E.F., DOUGHERTY B.A., MCKENNEY K., ADAMS M.D., LOFTUS B.,
RA PETERSON S., REICH C.I., MCNEIL L.K., BADGER J.H., GLODEK A., ZHOU L.,
RA OVERBECK R., GOICAYNE J.D., WEIDMAN J.F., McDONALD L., UTTERBACK T.,
RA COTTON M.D., SPRIGGS T., APTIACH P., KAINE B.P., SYKES S.M.,
RA SADOW P.W., D'ANDREA K.P., BORMAN C., FUJII C., GARLAND S.A.,
RA MASON T.M., OLSEN G.J., FRASER C.M., SMITH H.O., WOESE C.R.,
RA VENTER J.C.;
RT "The complete genome sequence of the hyperthermophilic,
RT sulphate-reducing archaeon Archaeoglobus fulgidus.";
RL NATURE 390:364-370(1997).
CC -!- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT
CC AMINOTRANSFERASES.
DR EMBL; AF000957; G2648397; -.
DR TIGR; AF2129; -.
DR PROSITE; PS00105; AA_TRANSFER_CLASS_1; 1.
DR PFAM; PF00155; aminotran_1; 1.
KW HYPOTHETICAL PROTEIN; TRANSFERASE; AMINOTRANSFERASE;
KW PYRIDOXAL PHOSPHATE.
SQ SEQUENCE 379 AA; 42699 MW; C0B47C9E CRC32;

Query Match 8.6%; Score 323; DB 1; Length 379;
Best Local Similarity 26.4%; Pred. No. 4.29e-32;
Matches 95; Conservative 95; Mismatches 143; Indels 27; Gaps 20;

Db 42 PDFTPTDFIIEAAYKAMKEGVF-YTPKGPVDELIDAVEIKLRNENGIDVGAENIIITPG 100
QY 182 PAFTAVEAEDAAVAVRTGQNCYPAGVGLPAARSVAEHLSCQVPYMLSADDVFLTAG 241
Db 101 AKYAIFAMCMLL-0EGDEVIILL-PSWVSVEA-CIL-MAGAKPVWVPHEGFE-D-API 154
QY 242 GTQAI-EVITPVLQTAGANILLPRPGYPNEYAFAFNLEVRHFDLIPDKGWEIDIDL 300
Db 155 EDYITNTKMWVNTPSNPLGVVPKFLKVRDLADKDLVMSDEIYKIIIFEGEHS 214
QY 301 ESTADKNTAMVLIINPNPCGSVSYDHLKVAEAKRILGILVIADENVYKLVLSAPFI 360
Db 215 LAAMGMLERTTINGFTSYMTGWRIGYAAPE-W-II---KLMNRQSH-SVS-HPT 267
QY 361 PMGVFGHTIPVLSIGSLKSVTPGWRLGWAVYDPKILQETKISTITNYLVNSTDPA 420
Db 268 SFVQYAGVAAL-KGDQSFKEIVEFRARRDMIMAKL-DEMGIEYAP-PKGAFYIFMNVG 324

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QY 421 TETQALPOILENTKEDFFKAIIGLLKESSEICVYKQIKENKYITCPHKPEGSMFVMVKLN 480
Db 325 -R-----DSN-EFCBEFLKREYVALTPGSAPGVAVKSNVRLSYATSRERIGEEFLSRLERE 377
QY 481 LHLLEEIDDDIDFCCKLAKEESVILCPGSLGMA--NWRITFACVPSLQDGLGRKISF 538

Search completed: Fri Oct 1 13:54:56 1999
Job time : 44 secs.

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